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STATISTICAL INFERENCE IN THE NON-PARAMETRIC CASE[1]

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CONTENTS

1. Introduction. In most of the problems of statistical inference for which we possess solutions the distribution function is assumed to depend in a known way on certain parameters. The values of the parameters are unknown, and the problems are to make inferences about the unknown parameter values. We refer to this as the parametric case. Under it falls all the theory based on normality assumptions.

Only a very small fraction of the extensive literature of mathematical statistics is devoted to the non-parametric case, and most of this is of the last decade. We may expect this branch to be rapidly explored however: The prospects of a theory freed from specific assumptions about the form of the population distribution should excite both the theoretician and the practitioner, since such a theory might combine elegance of structure with wide applicability. The process of development will no doubt inspire some mathematical attacks of considerable abstractness. There are already signs that more number-theoretic problems and measure-theoretic problems will enter our subject through this door, and perhaps even some topological ones. Some ability to think in terms of

[1] Parts of this paper were used in an invited address given under the title "Statistical inference when the form of the distribution function is unknown" before the meeting of the Institute of Mathematical Statistics on September 12, 1943 in New Brunswick, N. J.

functionals, function spaces, and metrization of function spaces will be useful in attempting general theories of "best" tests and estimates. Toward such abstract phases of the development the attitude of the practical statistician should be one of tolerance, for the new theory already promises to give him many new tools which are both simpler and of wider use.

While the maturity of the non-parametric theory is still in the future, it is well to remark that its beginnings go relatively far back. Of our most famous tests, such as Pearson's χ^2-test, Student's test, and Fisher's analysis of variance tests, the oldest concerns a non-parametric problem: In 1900 Karl Pearson proposed his χ^2-criterion to test the goodness of fit of a theoretical distribution to observations, and in 1911 he extended his χ^2-method to the problem of two samples. The first of these problems may be regarded as non-parametric if the choice of the theoretical distribution is not based on calculations from the data, and the second is without doubt a non-parametric problem. R. A. Fisher treated an analysis of variance problem non-parametrically at least as early as 1925, for in the first edition of his *Statistical Methods for Research Workers* we find the sign test. General formulations of the problems of statistical inference, and criteria for "good" and "best" solutions[2] have been advanced by R. A. Fisher, Neyman, E. S. Pearson, and Wald. These general theories were all strictly parametric until 1941 when Wald proposed one sufficiently broad to cover the non-parametric case.

We now introduce some notation to which we shall adhere throughout this paper. Statistical inferences are based on measurements. The total number of measurements will always be denoted by n. We conceive of n random variables $X_1, X_2, \cdots, X_n$ on which the measurements are made. The domain of each X_j can always be taken to be a set of real numbers. If vector random variables occur, the X_j will denote components. The cumulative distribution function (c.d.f.) of the random variables will be written $F_n(x_1, x_2, \cdots, x_n)$, —— this is the probability that all $X_j \leq x_j$ simultaneously. The c.d.f. F_n is then always defined in a complete n-dimensional Euclidean space W, called the sample space; W is the space of points $E = (x_1, x_2, \cdots, x_n)$. The sample point with the random coordinates $X_1, \cdots, X_n$ will be denoted by $\mathbf{E}$.

In describing the validity of specific non-parametric tests and estimates in the sequel it will be convenient to refer to the following classification[3] of *univariate* c.d.f's $F(x)$: Ω_0 is the class of all F. Ω_2 is the class of all continuous F. Ω_3 is the class of all absolutely continuous F, that is, those F for which there exists a probability density function $f(x)$, so that

$$F(x) = \int_{-\infty}^{x} f(\xi)\, d\xi.$$

Ω_4 consists of all F which may be written in the above form with f continuous.

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[2] For a bibliography see [22].

[3] The notation follows [31].

PART I. NON-PARAMETRIC TESTS

2. The randomization method of obtaining similar regions. In any problem of statistical inference it is assumed that the c.d.f. F_n of the measurements is a member of a given class Ω of n-variate distribution functions; we write $F_n \in \Omega$. Ω is called the class of admissible F_n. If Ω is a k-parameter family of functions the problem is called parametric, otherwise, non-parametric. A statistical hypothesis H is a statement that $F_n \in \omega$, where ω is a given subclass of Ω. A test of the hypothesis H consists of choosing a Borel region w in the sample space W and rejecting H if and only if the sample point $\mathbf{E}$ falls in w; w is called the critical region of the test.

The choice of the critical region w is usually[4] made as follows: A positive constant α (ordinarily about .01 or .05) is chosen and called the significance level of test. If regions w exist for which $Pr\{\mathbf{E} \in w \mid F_n\}$—the probability that the sample point $\mathbf{E}$ fall in w, calculated from the c.d.f. F_n—is equal to α for all $F_n \in \omega$, then the choice of critical region is usually limited to this class. Such regions are very important in the theory of testing hypotheses, and it is convenient to have a name for them: Following the terminology of Neyman [22] in the parametric case we shall call them *similar* to the sample space with respect to all F_n in ω, or more briefly, similar regions. A similar region is then a region w for which $Pr\{\mathbf{E} \in w \mid F_n\}$ is the same constant for all $F_n \in \omega$. The advantage of using similar regions as critical regions is that the risk of rejecting the hypothesis when it is true (type I error) is controlled: no matter what member of ω the unknown F_n happens to be, the probability of rejection of the (true) hypothesis is exactly α. We remark here that the problem of the existence and structure of similar regions in the parametric case has been treated only under very heavy restrictions and must be considered still mostly unsolved, whereas we shall see later that in the non-parametric case it promises to be relatively simple.

When similar regions exist for a chosen α there is usually a large family of them. Ideally the choice of the critical region w from the family of similar regions would be based on a complete knowledge of two functionals of F_n for $F_n \in \Omega - \omega$, that is, for those F_n corresponding to the various admissible ways in which the hypothesis can be false: the first, the probability of rejection (of avoiding a type II error), namely $Pr\{\mathbf{E} \in w \mid F_n\}$, called the power function of w, and the second, the relative importance of rejection in the concrete situation in which the test is to be applied. In other words, one would like to choose the w with the power function "best" for the very specific problem at hand. However, little has been done along this line in the non-parametric case, and, as we shall note below, the choice of w from the family of similar regions is usually made by means of a statistic chosen on intuitive grounds.

A general method of obtaining similar regions, which we shall call the *randomization method*, will now be described. The credit for originating this method and envisioning its wide applicability belongs to R. A. Fisher, who first

[4] Another approach to the choice of critical region will be described in section 13.

used it in 1925 [3]. Consider the set S of permutations on the coordinates $x_1, x_2, \cdots, x_n$, which leave invariant all the c.d.f's F_n in ω. Suppose the number of permutations in the set S is s; then s divides $n!$. Now define for any point E in W a corresponding set $\{E'\}$ of s points obtained by making on the coordinates of E the permutations of the set S. The value of the c.d.f. F_n is then the same at all s points E' generated by E, for all $E \in W$ and all $F_n \in \omega$. The s points of $\{E'\}$ will be distinct unless the point E lies in a certain region W_0; W_0 depends on the set S of permutations determined by the class ω, and will always be contained in the union of all diagonal hyper-planes $x_i = x_j$ $(i \neq j)$. A critical region w is constructed by the randomization method by choosing a positive integer $q < s$, and for every E not in W_0, putting q points of the corresponding set $\{E'\}$ in w and the remaining $s - q$ points outside w, by any rule whatever, just so w is a Borel set. We shall also say that a Borel set w is obtained by the randomization method if it has the structure just described except on a (Borel) subset w_0 of w having the property $Pr\{\mathbf{E} \in w_0 \mid F_n\} = 0$ for all $F_n \in \omega$. It may be shown by the methods used elsewhere [31] by the writer that if ω is a class of continuous c.d.f's then the region w thus obtained is a similar region with $\alpha = q/s$; furthermore, that under mild restrictions (roughly, that the boundary of w be a sufficiently "thin" set), at least for certain classes ω, this is the *only* method of obtaining similar regions.

One might call the set $\{E'\}$ of points corresponding to E the subpopulation of points "equally likely" under the null hypothesis H, but we shall call $\{E'\}$ simply the *subpopulation* corresponding to E. The decision as to which q of the s points of the subpopulation are to be put into the critical region w is usually made with the aid of a statistic T chosen on an intuitive basis. By a statistic T we mean of course a function of the sample only, not depending on the c.d.f. F_n, thus $T(\mathbf{E}) = T(X_1, \cdots, X_n)$. For a suitably chosen q, the q points of the subpopulation $\{E'\}$ giving $T(E')$ values in a certain range—usually the q largest or q smallest values—are put into w, and these q values are then called the "significant" values.

Before proceeding further let us consider an example illustrating all the definitions we have introduced thus far. Suppose that on the basis of a sample of m pairs (X_i, Y_i), $i = 1, 2, \cdots, m$, from a bivariate population with unknown c.d.f $G(x, y)$ we wish to test the independence of the random variables X, Y. To fit our general notation write $Y_i = X_{i+m}$. Assuming only that the sample is random, we have, with $n = 2m$, that the c.d.f. of the sample point $\mathbf{E}$ is of the form

$$F_n(x_1, \cdots, x_n) = \prod_{i=1}^{m} G(x_i, x_{i+m}).$$

Now suppose we know or are willing to assume further that the unknown c.d.f. $G(x, y)$ of the population is in a certain class $\Omega_\nu^{(2)}$ of bivariate c.d.f.'s, where $\Omega_\nu^{(2)}$ is the bivariate analogue of the class Ω_ν of univariate c.d.f.'s defined in section

1; thus if we knew the unknown $G(x, y)$ were continuous, we would have $G \in \Omega_2^{(2)}$. The class Ω of admissible F_n is then

$$\Omega = \left\{ F_n \mid F_n = \prod_{i=1}^{m} G(x_i, x_{i+m}); G \in \Omega_\nu^{(2)} \right\},$$

where the notation $\{F_n \mid F_n \text{ of the form } \mathfrak{F}\}$ denotes the class of all F_n of the form $\mathfrak{F}$. The hypothesis of independence may now be expressed as $H: F_n \in \omega$, where the subclass ω of Ω is

$$\omega = \left\{ F_n \mid F_n = \prod_{i=1}^{m} F^{(1)}(x_i) \prod_{j=m+1}^{2m} F^{(2)}(x_j); F^{(k)} \in \Omega_\nu, k = 1, 2 \right\}.$$

The set S of permutations which leave all $F_n \in \omega$ invariant is obtained by making all possible permutations of the first m coordinates $x_1, \cdots, x_m$ among themselves, and of the second m coordinates $x_{m+1}, \cdots, x_{2m}$ among themselves. The total number s of permutations in S is thus $(m!)^2$. Making these permutations on the coordinates of any point E in W, we get the set $\{E'\}$ of $(m!)^2$ points. The points of $\{E'\}$ are distinct unless E lies in the region W_0 defined as the union of all hyperplanes $x_i = x_j$ where $i \neq j$ and i, j are both in the set of integers $1, 2, \cdots, m$ or else both in the set $m + 1, \cdots, 2m$. Pitman [28] applied the randomization method to this problem, using as the statistic $T(E)$ the numerical value of the (sample) Pearsonian correlation coefficient,

$$T(E) = \left| \sum_{i=1}^{m} x_i x_{i+m} \right| \Big/ \left(\sum_{i=1}^{m} x_i^2 \sum_{j=m+1}^{2m} x_j^2 \right)^{\frac{1}{2}},$$

the large values of T being the significant ones. We note that $T(E)$ takes on at most $m!$ different values over the subpopulation. What we previously called a "suitably chosen" q would be in the present case a multiple of $m!$, and the choice of significance level $\alpha = q/s$ would then be limited to multiples of $1/m!$.

The method of randomization is seen to exploit whatever symmetry properties the F_n in ω possess as a class. A special case of the general method is the *method of ranks*. This gives regions of an especially simple form defined by certain inequalities on the coordinates. Probably the only case in which the method of ranks will ever be used is when the F_n in ω have the following special kind of symmetry: Suppose they are completely symmetrical in each of certain subsets of the coordinates, say t sets of $n_1, n_2, \cdots, n_t$ coordinates, respectively, where $\sum_{i=1}^{t} n_i = n$. We may assume the coordinates numbered so that F_n is completely symmetrical in the set $x_{p_i+1}, x_{p_i+2}, \cdots, x_{p_i+n_i}$ $(p_i = \sum_{j=1}^{i-1} n_j; i = 2, 3, \cdots, t; p_1 = 0)$, for all $F_n \in \omega$. The set S of permutations is thus generated by making all $n_i!$ permutations on the n_i coordinates $x_{p_i+1}, \cdots, x_{p_i+n_i}$ $(i = 1, \cdots, t)$, so that the total number of permutations in S is $s = n_1!\, n_2! \cdots n_t!$.

Corresponding to the i-th set of coordinates in which F_n is symmetrical, let us divide the sample space W up into $n_i!$ regions defined by

$$x_{p_i+1} < x_{p_i+2} < \cdots < x_{p_i+n_i}$$

and the $n_i! - 1$ other inequalities obtained by permuting the subscripts in the above. Denote these regions by $w_{i,k}$ $(k = 1, \cdots, n_i!)$. Let

$$w_{k_1,k_2,\cdots,k_t} = w_{1,k_1} \cap w_{2,k_2} \cap \cdots \cap w_{t,k_t},$$

that is, $w_{k_1,k_2,\cdots,k_t}$ is the part of W common to the regions $w_{1,k_1}, w_{2,k_2}, \cdots, w_{t,k_t}$. This process divides the sample space W up into s disjoint regions $w_{k_1,k_2,\cdots,k_t}$, which we shall now denote simply by w_σ $(\sigma = 1, \cdots, s)$. The set $\{w_\sigma\}$ of regions covers all of the sample space W except the region W_0 on which certain coordinates become equal. We shall say that the sample point $\mathbf{E}$ has the σ-th ranking, R_σ, if $\mathbf{E}$ falls in w_σ. We may then speak of a random variable $R = R(\mathbf{E})$, the "ranking", taking on the s possible values R_σ, or the "tied" ranking R_0 if $\mathbf{E} \in W_0$.

A critical region w is constructed by the method of ranks by taking w to be the union of q of the regions w_σ. Those rankings R_σ corresponding to the q regions w_σ constituting the critical region w, will be called the significant rankings. Any statistic $T(E)$ used as the criterion to decide which are the significant rankings now becomes a function of the ranking R only, $T(E) = U(R)$. We may regard the method of ranks as a simplification of the problem of testing statistical hypotheses, in which the infinite n-dimensional sample space W is replaced by a finite space of $s + 1$ points R_σ. If Ω is a class of continuous F_n we may ignore the point R_0 since then $Pr\{R = R_0\} = 0$.

In the problem of independence, which we have used before to illustrate the definitions of this section, the method of ranks was applied by Hotelling and Pabst [9], who took as the statistic $U(R)$ the numerical value of the Spearman coefficient of rank correlation, large values being significant.

The method of randomization yields similar regions if ω is a class of continuous functions. What will the method get us if we drop the continuity restriction? In this case we can no longer ignore the possibility that the sample point $\mathbf{E}$ fall in the exceptional region W_0, for we do not have $Pr\{\mathbf{E} \in W_0\} = 0$. We owe to Pitman [27] the following idea: We continue to use the subpopulation $\{E'\}$ and a chosen statistic $T(E)$ as above, but instead of separating the points of $\{E'\}$ into two classes (significant points and non-significant points) by means of $T(E)$ we now add a third class of "doubtful" points.[5] If the s points of the set $\{E'\}$ are not distinct they are to be counted according to their multiplicities under the process of applying the permutations of the set S to the coordinates of E. Suppose that the large values of T are significant. Number the s points of $\{E'\}$ so that $T(E'_1) \geq T(E'_2) \geq \cdots \geq T(E'_s)$. If $T(E'_q) > T(E'_{q+1})$ we call $E'_1, \cdots, E'_q$ significant, and the rest non-significant. However if $T(E'_q) = T(E'_{q+1})$, we term all points E' with $T(E') = T(E'_q)$ doubtful, points E' for which $T(E') > T(E'_q)$, significant, and points E' with $T(E') < T(E'_q)$, non-significant. This process divides the sample space W up into three regions instead of the customary

[5] Instead of the terms significant, non-significant, doubtful, Pitman uses discordant, concordant, neutral.

two, namely, a rejection region w_R, an acceptance region w_A, and a doubtful region w_D. It is a special case of the following procedure: For every set $\{E'\}$ define positive integers $m_R = m_R(\{E'\})$ and $m_A = m_A(\{E'\})$ such that $m_R \leq q$, $m_A \leq s - q$, and put m_R of the points E' in w_R, m_A of the points E' in w_A, and the remaining $s - m_A - m_R$ of the points E' in w_D, in any way so that w_R and w_A are Borel regions. When any E' is assigned to w_R or w_A it is to be counted according to its multiplicity as defined above, if $\{E'\}$ contains less than s distinct points. It may be shown that with $\alpha = q/s$, $Pr\{\mathbf{E} \in w_R \mid F_n\} \leq \alpha$ and $Pr\{\mathbf{E} \in w_A \mid F_n\} \leq 1 - \alpha$ for all $F_n \in \omega$, that is, whenever H is true.

Before closing this section on the method of randomization, we mention a few difficulties which frequently arise when it is applied. Except for very small samples the calculation determining whether or not the observed value E_0 of the sample point $\mathbf{E}$ belongs to the significant points of the subpopulation $\{E_0'\}$ generated by E_0, is usually extremely tedious. In such cases the author of the test often gives an approximation to the discrete distribution of his statistic $T(\mathbf{E})$ over the subpopulation $\{E'\}$ by means of some familiar continuous distribution for which tables are available, the laborious exact calculation by enumeration then being replaced by the computation of a few moments (that is, values of certain homogeneous polynomials in the observed coordinates) and the use of existing tables of percentage points of the continuous distribution.[6] Barring some papers where the method of ranks is used, the justification of these approximations is never satisfactory from a mathematical point of view, the argument being based on a study of the behavior of two, or at most four, moments. The only exception to the last statement appears to be a very recent paper by Wald and Wolfowitz [42], which may point the way to genuine derivations of asymptotic distributions for the non-rank case of the randomization method. We shall distinguish between derivations of asymptotic distributions and arguments based on two or four moments by saying that a distribution is "proved" in the former case and "fitted" in the latter.

Another difficulty arises, most noticeably in the method of ranks, out of the possibility of equality of the observed coordinates. In the distribution theory this is usually avoided by assuming ω to be a class of continuous c.d.f's, so that $Pr\{\mathbf{E} \in W_0 \mid F_n\} = 0$ for all $F_n \in \omega$, but in practice, since the measurements are usually made to about three significant figures, ties *do* occur in the sample. While some scattered work has been done on this question there is need for a thorough general treatment.

In some of the work that has been done on particular non-parametric tests

[6] In many cases the approximate test obtained by fitting a familiar distribution is found to coincide with widely used tests based on normality assumptions. In such cases if the fitting is asymptotically correct the following remarks are justified: (1) If the non-parametric test is used in a case where we hesitate to assume normality but normality actually exists, the non-parametric test is asymptotically as efficient as the older test assuming normality. (2) If normality is assumed when it does not exist, no error is incurred asymptotically when the older test is used.

it is not very clear just what the null hypothesis H is. Two situations often occur: Suppose $H: F_n \in \omega$ is the hypothesis we actually wish to test at significance level α. Let w be the chosen critical region and ω_w the class of F_n for which $Pr\{\mathbf{E} \in w \mid F_n\} = \alpha$. The two situations are (*i*) ω is a proper subset of ω_w, and (*ii*) ω_w is a proper subset of ω. Of these (*i*) seems less objectionable, for then the probability of a type I error (rejecting H when true) is strictly α, but the probability of accepting H is the same when certain alternatives ($F_n \in \omega_w - \omega$) are true as when H is true. In case (*ii*) the probability of a type I error is not α unless F_n is in the subclass ω_w of ω; thus there might be a much higher probability than α of rejecting H when it is true, if the true $F_n \in \omega - \omega_w$. To illustrate situation (*i*) consider K. Pearson's χ^2-test for goodness of fit of a theoretical distribution $F_0(x)$ to a sample $\mathbf{E}$. Suppose $\mathbf{E}$ is from a univariate population whose true c.d.f. is $F(x)$. If F has the property that for the intervals I_j defined in section 3, $\int_{I_j} dF = \int_{I_j} dF_0$, $j = 1, 2, \cdots, N$, then the probability of rejection is the same as when the hypothesis is true. An example of (*ii*) might occur if we wish to test whether the *means* of two univariate populations are the same. If we use one of the tests of section 4 in which the probability of rejection is calculated under the assumption that the *distributions* of the populations are the same, then we do not know that the probability of a type I error is α, for the samples might come from two populations with the same mean but different distributions.

3. Goodness of fit. Randomness. The non-parametric case of testing goodness of fit is the following: On the basis of a sample $\mathbf{E}$ from a population with c.d.f. $F(x)$ known to be a member of some Ω_r, we wish to test whether $F = F_0$, where F_0 is a given c.d.f. The class of admissible c.d.f.'s F_n is

$$\Omega = \left\{F_n \mid F_n = \prod_{i=1}^{n} F(x_i);\ F \in \Omega_r\right\},$$

and the hypothesis H specifies that $F_n \in \omega$, where

$$\omega = \left\{F_n \mid F_n = \prod_{i=1}^{n} F_0(x_i)\right\}.$$

K. Pearson's χ^2-test [25] consists of choosing an integer N, dividing the x-axis up into a set $\{I_j\}$ of disjoint intervals ($j = 1, 2, \cdots, N$), and using as statistic $T(E)$ the Pearsonian chi square,

$$\chi_P^2 = \sum_{j=1}^{N} [m_j - \mathcal{E}(m_j)]^2 / \mathcal{E}(m_j),$$

where m_j is the number of observed coordinates of $\mathbf{E}$ in I_j, and $\mathcal{E}(m_j) = n\int_{I_j} dF_0$. Large values of χ_P^2 are regarded as significant. Exact significance

levels for χ_P^2 could be obtained by considering its distribution over the subpopulation $\{E'\}$ generated by the sample. This process would lead to the multinomial distribution of the m_j mentioned in the usual derivations of the asymptotic distribution of χ_P^2 (for $n \to \infty$ with N fixed). Pearson himself found this asymptotic distribution, namely the χ^2-distribution with $N - 1$ degrees of freedom. In studying the problem of a "best" choice of the set $\{I_j\}$ of intervals, Mann and Wald [17] adopted a non-parametric treatment, with $\nu = 2$ for the class Ω_ν above.

Another test not depending on a choice of intervals I_j could be made by using confidence belts for F as described in section 9 and rejecting H at the α level of significance if the graph of F_0 is not covered by the belt with confidence coefficient $1 - \alpha$.

The problem of randomness is usually non-parametric; in the univariate case the class ω of this problem is identical with the class Ω of the preceding. The index ν and the class Ω for the problem of randomness would depend on the specific situation in which it arises. With two exceptions [42, 52], all tests of randomness proposed thus far have been functions of runs in the sample. Two kinds of runs have been considered, runs up and down, and runs above and below the median [1, 4, 14, 19, 32, 44, 51]. We note that the set S of permutations determined by ω is the set of all $n!$ permutations on the n coordinates of E. Suppose now $\nu = 2$. The proof [31] that all similar regions w have the randomization structure applies to this problem. On the other hand such a region w has the property $Pr\{\mathbf{E} \in w \mid F_n\} = \alpha$ for any F_n which is completely symmetrical in the coordinates. Difficulty (i) discussed at the end of section 2 now arises if Ω contains such symmetrical alternatives. The definition of an appropriate class $\Omega - \omega$ of alternatives and the question of the power of tests against the alternatives make the problem of randomness a difficult one. Beyond these few remarks we refer the reader to an expository paper by Wolfowitz [51] devoted to the problem in the previous issue of this journal, and to a paper by Wald and Wolfowitz [42] in the present issue. The latter paper is one of the exceptions, previously mentioned, not based on the method of ranks.

4. The problem of two samples. Suppose $X_1, \cdots, X_{m_1}$ and $Y_1, \cdots, Y_{m_2}$ are samples from univariate populations with c.d.f's $F(x)$ and $G(x)$ respectively, where we assume $F, G \in \Omega_\nu$, and that we wish to test the hypothesis that $F = G$. Write $Y_i = X_{i+m_1}$, so that with $n = m_1 + m_2$ we have

$$\Omega = \left\{F_n \mid F_n = \prod_{i=1}^{m_1} F(x_i) \cdot \prod_{j=m_1+1}^{n} G(x_j);\ F, G \in \Omega_\nu\right\},$$

$$\omega = \left\{F_n \mid F_n = \prod_{i=1}^{n} F(x_i);\ F \in \Omega_\nu\right\}.$$

The set S of permutations determining the subpopulation $\{E'\}$ consists of all $n!$ permutations on the n coordinates of E. The writer has shown [31] that no

similar regions exist in this case if $\nu = 0$, while if $\nu = 2$, 3, or 4 a similar region necessarily has the randomization structure.

The first non-parametric attack on this problem was given [26] by K. Pearson. The x-axis is divided up into intervals $I_1, \cdots, I_N$ as in section 3. Let m_{j1} and m_{j2} be the number of measurements from the first and second samples, respectively, falling in I_j, so that $\sum_{j=1}^{N} m_{jk} = m_k$, $k = 1, 2$. The statistic $T(E)$ used is

$$\chi^2_{P'} = (m_1 m_2)^{-1} \sum_{j=1}^{N} (m_1 m_{j2} - m_2 m_{j1})^2/(m_{j1} + m_{j2}),$$

with large values significant. In view of the remarks at the end of the last paragraph it would be necessary to calculate the distribution of $\chi^2_{P'}$ over the subpopulation $\{E'\}$ in order to get a similar region. Pearson found the asymptotic distribution of $\chi^2_{P'}$ under the null hypothesis to be the χ^2-distribution with $N - 1$ degrees of freedom.

A solution based on the method of randomization was proposed by Pitman [27]; the special case of this solution for $m_1 = m_2$ was published a little earlier by R. A. Fisher [6]. Pitman employed the numerical value of the difference of the sample means as statistic,

$$T(E) = \left| \sum_{i=1}^{m_1} x_i/m_1 - \sum_{j=m_1+1}^{n} x_j/m_2 \right|,$$

large values being significant. He fitted an incomplete Beta-distribution to the subpopulation distribution of his $T(E)$, and noted that this approximation gave a result identical with the usual t-test valid when the population distributions $F(x)$ and $G(x)$ are assumed normal with equal variances.

Turning now to tests based on the method of ranks, we mention here that one for the case $m_1 = m_2$ was given by R. A. Fisher as early as 1925, namely the "sign test" or "binomial series test" [3]. We may (and Fisher did) regard this as a test of a less restrictive hypothesis, and shall describe it in section 6. Between 1938 and 1940 several tests employing ranks were proposed for the problem of two samples. The earliest of these, by W. R. Thompson [36], was shown to be inconsistent (section 11) with respect to certain alternatives $F_n \epsilon \Omega - \omega$ by Wald and Wolfowitz [40]. These authors used as statistic $U(R)$ the total number of runs in a sequence V of n elements constructed as follows: Rank the measurements of the combined sample in order of increasing magnitude. According as the j-th measurement in this rank order is from the first or second sample, put the j-th element of the sequence V equal to 1 or 2. In this test small values of the statistic $U(R)$ are regarded as significant. The test is now quite practicable (for $\nu = 2$) for certain ranges of m_1 and m_2. For m_1 and m_2 both ≤ 20, tables by Swed and Eisenhart [34] give the 1% and 5% significant values of $U(R)$. Wald and Wolfowitz proved that for $n \to \infty$ with $k = m_1/m_2$ fixed, the distribution of $U(R)$ is asymptotically normal with mean $2m_1/(1 + k)$ and variance $4km_1/(1 + k)^3$. Swed and Eisenhart computed that for $m_1 = m_2$ this

gives a very satisfactory approximation outside the range of their tables. However, further computation needs to be done on the accuracy of this approximation for $m_1 \neq m_2$ and one of them >20.

Another test based on ranks was advanced by Dixon [2], using as statistic $U(R)$ the random variable

$$C^2 = \sum_{j=1}^{m_1+1} [(m_1 + 1)^{-1} - n_j/m_2]^2,$$

where the integers n_j are defined thus: Let $Z_1 \leq Z_2 \leq \cdots \leq Z_{m_1}$ denote the measurements of the first sample arranged in rank order. Then n_j is the number of measurements in the second sample falling in the interval (Z_{j-1}, Z_j), where we define $Z_0 = -\infty$, $Z_{m_1+1} = +\infty$. Large values of C^2 are significant. Dixon tabulated the 1%, 5%, and 10% significant values of C^2 for $m_1, m_2 = 2, 3, \cdots, 10$; for larger m_1, m_2 he fitted a χ^2-distribution.

A paper by Smirnoff [33, 16] suggests the following as a statistic $U(R)$: Let $G_{m_1}(x)$ and $G_{m_2}(x)$ be the "empirical distribution functions" of the first and second samples, that is, $m_i G_{m_i}(x)$ is the number of measurements in the i-th sample $\leq x$ $(i = 1, 2)$ and take[7]

$$U(R) = (m_1^{-1} + m_2^{-1})^{-1} \sup_x |G_{m_1}(x) - G_{m_2}(x)|$$

with large values significant. Smirnoff showed that if $\nu = 2$ the asymptotic distribution of his statistic $U(R)$ is a certain c.d.f. $\Phi(\lambda)$, previously introduced by Kolmogoroff [15]. More specifically, let $\Phi_{m_1,m_2}(\lambda) = Pr\{U(R) \leq \lambda; \nu = 2\}$. Then if $n \to \infty$ with m_1/m_2 fixed, we have $\Phi_{m_1,m_2}(\lambda) \to \Phi(\lambda)$. The definition of $\Phi(\lambda)$ and references to tables of $\Phi(\lambda)$ are given in section 9. If instead of assuming $\nu = 2$ we take $\nu = 0$, the risk of type I errors may be controlled to the extent that $Pr\{\text{rejecting } H\} \leq \alpha$ for all $F_n \in \omega$, by employing Smirnoff's theorem stating $Pr\{U(R) \leq \lambda; \nu = 0\} \leq \Phi_{m_1,m_2}(\lambda)$, where $\Phi_{m_1,m_2}(\lambda)$ is defined above.

A test for the problem of two samples obtained by Wolfowitz by a modification of the likelihood ratio procedure will be discussed in section 12. When $m_1 = m_2$ the non-parametric analysis of variance tests of the "randomized blocks" type described in section 6 might also be used to test the more restricted hypothesis considered in this section.

The non-parametric problem of k samples has been attacked by Welch [46], who used the method of randomization with the analysis of variance ratio as statistic $T(E)$, and by Wolfowitz [50] with his modified likelihood ratio method.

In this as in all the other sections where several solutions of the same problem of statistical inference are described, the question as to the relative merits of the various solutions arises, and in every case the question is as yet mostly or entirely unanswered. The only easy conclusion about the tests of this section would seem to be that the tests of K. Pearson and Pitman are not consistent with

[7] We use the notations *sup* and *inf* respectively for least upper bound and greatest lower bound.

respect to certain subclasses of the admissible alternatives, according to the definition of section 11.

5. Independence. The classes Ω and ω defining the problem of independence have already been stated in section 2, in which we described Pitman's test [28] based on the randomization method and the use of $|r|$ as statistic $T(E)$, where r is the sample value of the Pearsonian correlation coefficient. Pitman fitted an incomplete Beta-distribution to the subpopulation distribution of r^2 and found the resulting approximation for $\nu = 2$ equivalent to the usual test employing the t-distribution and valid for the case of normality.

In section 2 we also mentioned the test earlier proposed by Hotelling and Pabst [9], which is based on the method ranks and employs the statistic $U(R) = |r'|$, where r' is the Spearman rank correlation coefficient. They proved that for $\nu = 2$ the distribution of r' is asymptotically normal if $F_n \epsilon \omega$. Pitman's fitting of an incomplete Beta-distribution applies also to $(r')^2$, and Kendall, Kendall, and Smith [12] made numerical calculations indicating that this gives a better approximation than the normal distribution. Since r' is calculated from Σd^2, the sum of the squared rank differences, the latter may equivalently be used as the statistic $U(R)$, small and large values of Σd^2 being now both significant. Kendall, Kendall, and Smith [12] found the exact distribution of Σd^2 for the number of pairs $m \leq 8$. This work was anticipated by Olds [23], who calculated the exact distribution of Σd^2 for $m \leq 7$, and by fitting certain distributions for $m > 7$, gave a very useful table of the 1%, 2%, 4%, 10% and 20% significant values of Σd^2 for $m \leq 30$. It would be desirable to have these tables extended by inclusion of the 5% values.

M. G. Kendall [10] proposed another measure of rank correlation whose significant values are easier to calculate than those of Σd^2, but since the Olds' tables for the latter are available, Kendall's innovation does not seem to possess much practical advantage. Wolfowitz [50], using his modified likelihood ratio method, gave another test for independence and generalized it to the problem of independence of k random variables.

6. Analysis of variance. We suppose that we have $n = rc$ measurements arranged in a rectangular layout of r rows and c columns. The r rows might correspond to the blocks and the c columns to the varieties in an agricultural experiment. The null hypothesis H is that of "no difference" in the column effects. The measurement in the i-th row and j-th column is supposed to be on a random variable[8] X_{ij} with c.d.f. $F^{(ij)}(x) = Pr\{X_{ij} \leq x\}$. Let us assume at first that all the X_{ij} are independent. The joint c.d.f. of the random variables $X_{1j}, \cdots, X_{rj}$ of the j-th column is then

$$F^{(j)}(x_1, \cdots, x_r) = Pr\{x_{1j} \leq x_1, \cdots, x_{rj} \leq x_r\} = \prod_{i=1}^{r} F^{(ij)}(x_i).$$

[8] The double subscript notation is more convenient here than that used in section 2; after the class ω has been defined the reader will see that the numbers n_i used in section 2 to describe the symmetry of the $F_n \epsilon \omega$ are all equal to c, and the X_{ij} of the present section coincides with the X_{pi+j} of section 2.

The symbol F_n for the joint c.d.f. of all n random variables now denotes $F_n(x_{11}, \cdots, x_{1c}; \cdots; x_{r1}, \cdots, x_{rc})$. Ω is the class of all F_n of the form

$$F_n = \prod_{j=1}^{c} F^{(j)}(x_{1j}, \cdots, x_{rj}),$$

where $F^{(j)}$ is defined by the preceding equation, and all $F^{(ij)}$ are in a given class Ω_r. The hypothesis H states that the column distributions are all the same,

$$F^{(j)}(x_1, \cdots, x_r) = F^{(1)}(x_1, \cdots, x_r) \qquad (j = 2, 3, \cdots, c),$$

without specifying $F^{(1)}$. ω is thus the subclass of Ω comprising all F_n of the form

$$F_n = \prod_{j=1}^{c} F^{(1)}(x_{1j}, \cdots, x_{rj}).$$

The F_n in ω may be written

$$F_n = \prod_{i=1}^{r} \left\{ \prod_{j=1}^{c} F^{(i1)}(x_{ij}) \right\}.$$

Regarding the factor in braces for fixed i, we see that it is left unchanged by any permutation of the c coordinates $x_{i1}, \cdots, x_{ic}$. The set S of permutations is thus determined, and the subpopulation $\{E'\}$ consists of the $(c!)^r$ points obtained by permuting among themselves the first set of c coordinates, the second set of c coordinates, $\cdots$, the r-th set of c coordinates of $E = (x_{11}, \cdots, x_{1c}; \cdots; x_{r1}, \cdots, x_{rc})$.

The above argument leading to the subpopulation $\{E'\}$ of $(c!)^r$ points is based squarely on the assumed independence of the n random variables X_{ij}. Suppose now that the X_{ij} are not known to be independent, as may happen in agricultural experiments [24]. To make the discussion concrete suppose in the $r \times c$ layout we have been considering, the rows refer to blocks (of plots) and the columns to varieties, so that the random variable X_{ij} is the yield of the j-th variety on the i-th block. We owe to R. A. Fisher the method of including early in the experiment a random process which leads to the same "equally likely" subpopulation of points $\{E'\}$ obtained before in the case of independence. This physical process which he calls "randomization" then permits the construction of critical regions by the "method of randomization" in the sense we have been using the term.

To explain the experimental process of randomization we shall imagine another $r \times c$ layout and a random set of mappings of the two layouts onto each other. In each block there are c plots and we now assume these numbered from 1 to c, the numbering to be held fixed. The second layout refers to the plots; the rows again correspond to the blocks, but the columns now correspond to the number of the plot in the block, thus the i, j cell represents the j-th plot in the i-th block. Now consider all 1:1 correspondences or mappings between the two layouts so that the i-th row always maps onto the i-th row $(i = 1, \cdots, r)$. There are $s = (c!)^r$ such mappings M_k $(k = 1, \cdots, s)$. Suppose under the mapping M_k the i, t cell in the block-plot layout maps on the i, j_k cell of the block-variety

layout, where $j_k = j_k(i, t)$, and the i, j cell of the latter corresponds to the i, t_k cell of the former, $t_k = t_k(i, j)$. The physical randomization process consists of choosing the mapping M_k so that all s mappings have the same probability $1/s$ of being chosen. In other words, the randomized block pattern is selected in such a way that all the s possible patterns have equal probabilities of being adopted in the experiment. Now let $Y_{it}^{(k)}$ be the yield of the i, t plot if the variety assigned to it by the k-th pattern is planted there, and let $G^{(k)}(y_{11}, \cdots, y_{rc}) = Pr\{\text{all } Y_{ij}^{(k)} \leq y_{ij}\}$ be the joint c.d.f. of the $Y_{ij}^{(k)}$. In calculating the c.d.f. F_n of the X_{ij} associated with the first layout we must take account of the random process by which it is mapped onto the second:

$$\begin{aligned} F_n(x_{11}, \cdots, x_{rc}) &= Pr\{\text{all } X_{ij} \leq x_{ij}\} \\ &= \sum_{k=1}^{s} Pr\{\text{all } X_{ij} = Y_{i,t_k(i,j)}^{(k)}\}\ Pr\{Y_{i,t_k(i,j)}^{(k)} \leq x_{ij}\} \\ &= \sum_{k=1}^{s} s^{-1} G^{(k)}(x_{1,t_k(1,1)}, \cdots, x_{r,t_k(r,c)}). \end{aligned}$$

Ω consists of all F_n of the above form with $G^{(k)}$ in a given class, say $\Omega_\nu^{(n)}$. The hypothesis H of "no difference" of varieties asserts that the yields of the plots do not depend on the varieties planted on them, that is, that all $G^{(k)}$ are the same, $G^{(k)} = G^{(1)}$, without specifying $G^{(1)}$. ω is the subclass of Ω whose members are of the form

$$F_n = s^{-1} \sum_{k=1}^{s} G^{(1)}(x_{1,t_k(1,1)}, \cdots, x_{r,t_k(r,c)}).$$

It is now seen that any permutation in the set S previously considered merely rearranges the terms of the above sum, so that F_n remains invariant, and we have the same subpopulation $\{E'\}$ as before.

It is to be understood henceforth that either the X_{ij} are known to be independent or else an experimental randomization has been carried out as described above, so that in either case the above set $\{E'\}$ of $(c!)^r$ points is the "equally likely" subpopulation.

The first application in the literature of the randomization method is found in R. A. Fisher's "sign test" or "binomial series test" [3] for the case of randomized blocks with two columns ($c = 2$). Let D_i be the difference $X_{i1} - X_{i2}$. The statistic used is a function of the ranking only, namely the number of $D_i > 0$, small and large values being significant. For $\nu = 2$ its distribution under the null hypothesis is the binomial distribution with the n and p of the usual notation equal respectively to r and $\frac{1}{2}$. This test may be regarded as the special case when $c = 2$ of Friedman's rank method for analysis of variance to be described below.

Fisher later [5] proposed another test for the case $c = 2$ not based on ranks, and employing as statistic $T(E)$ the absolute value of the mean of the D_i defined above, with large values significant. The exact distribution of this statistic is very laborious to calculate unless r is very small, and K. R. Nair [20] pointed

out that the use of the numerical value of the median of the D_i (or one of the two central values when r is even) had the advantage of a very easily calculated distribution (if $\nu = 2$). The latter may be regarded as a modification of the rank method, the method of ranks being applied not in the $2r$-dimensionsl sample space as described in section 2 but in the r-dimensional space of the differences D_i. Nair also showed that the distributions of the range and of the midpoint of the range of the D_i are very simple.

From here on we consider the general case $c \geq 2$, but when we speak of distributions they will be understood to be for the case when the null hypothesis is true and $\nu = 2$. Welch [45] considered using as $T(E)$ the usual analysis of variance ratio appropriate to testing for "no difference" of column effects. He transformed this to another statistic and calculated two moments of its subpopulation distribution. The first moment always agrees with that obtained under "normal theory", that is for the case $X_{ij} = C_i + Z_{ij}$, where the C_i are constants and the Z_{ij} are independently normally distributed with the same variance and zero means, but the second moment depends on the subpopulation $\{E'\}$. Here the exact distribution of the statistic is of course in general much more tedious to calculate than in the previous case $c = 2$; an incomplete Beta-distribution was fitted by Welch. Welch anticipated Pitman [29] who obtained the same results and got besides the third and fourth moments of Welch's statistic.

The method of ranks was applied by Friedman [7] who employed as statistic $U(R)$ a quantity formed as follows: Rank each set of row entries X_{ij} (for fixed i) in ascending order of magnitude, and let r_{ij} be the rank of X_{ij}, so that $r_{i1}, \cdots, r_{ic}$ is a rearrangement of the integers $1, \cdots, c$. Let $\bar{r}_j$ be the mean rank of the j-th column, $\bar{r}_j = \sum_{i=1}^{r} r_{ij}/r$, and take for $U(R)$

$$U = C_{rc} \sum_{j=1}^{c} [\bar{r}_j - \mathfrak{E}(\bar{r}_j)]^2,$$

where C_{rc} is a certain constant, and $\mathfrak{E}(\bar{r}_j)$ is calculated under the null hypothesis. For Friedman's choice of C_{rc}, U may be rapidly computed from the equivalent formula

$$U = -3r(c+1) + 12 \sum_{j=1}^{c} \left(\sum_{i=1}^{r} r_{ij} \right)^2 \Big/ [rc(c+1)].$$

In his paper Friedman included a proof of Wilks' that U has asymptotically the χ^2-distribution with $c - 1$ degrees of freedom as $r \to \infty$. Kendall and Smith [13] fitted to a transform of U a Fisher z-distribution with continuity corrections, obtaining a better approximation for small r than the χ^2-distribution. Wallis [43] independently proposed the use of $\eta_r^2 = U/[r(c-1)]$ as statistic and called it the rank correlation ratio. Friedman in a later paper [8] on the subject, using exact values he had calculated, together with the Kendall-Smith approximation, published tables[9] of the 1% and 5% significant values of U for $c = 3, 4, 5, 6,$

[9] In these tables our U, r, c are denoted respectively by χ_r^2, m, n.

7, and sufficiently many values of r so that for these c and any r the significant values of U are now easily available.

After the above lengthy discussion for the "randomized blocks" case of analysis of variance, it will perhaps suffice merely to mention that the "Latin square" case may be similarly attacked from the non-parametric point of view, and this has been considered by Welch [45], Pitman [29], and E. S. Pearson [24]. They have taken as the statistic the usual analysis of variance ratio, and the work of Welch and Pitman in calculating the first two moments of its subpopulation distribution is even more tedious than in the "randomized blocks" case.

Part II. Non-parametric Estimation

7. Classical results on point estimation. Throughout part II the symbol $\mathbf{E}$ will always denote a random sample $X_1, \cdots, X_n$ from a univariate population with c.d.f. $F(x)$, where F is an unknown member of a given class to be stated in each case. The c.d.f. of $\mathbf{E}$ is thus

$$F_n(x_1, \cdots, x_n) = \prod_{i=1}^{n} F(x_i).$$

The problems of estimation can be stated without reference to the class Ω of admissible F_n; Ω would be obvious in every case.

Let $\theta = \theta(F)$ be a real number determined by F (a functional of F) for F in a certain class of univariate c.d.f's. Thus θ might be the mean of the distribution, in which case θ would be defined for all F possessing a first moment. We shall not call θ a parameter in order to avoid confusion with the parametric case. R. A. Fisher's criteria of unbiasedness and of consistency for point estimation carry over without change from the parametric case. A statistic $T(E)$ is said to be an unbiased estimate of θ if $\mathfrak{E}(T) = \theta$. Write $\mathbf{E} = \mathbf{E}_n$ and $T = T_n$ to emphasize the sample size n, and assume that the statistic $T_n(\mathbf{E}_n)$ is defined for all n (or all $n >$ some n_0). Then we define $T_n(\mathbf{E}_n)$ to be a consistent estimate of θ if it converges stochastically to θ, that is, if $Pr\{| T_n - \theta | > h\} \to 0$ as $n \to \infty$, for every $h > 0$.

In the present paragraph it will be convenient to symbolize the class of F for which the i-th (absolute) moment exists; we denote it by $\Omega_{(i)} (i = 1, 2, \cdots)$. It is known[10] that a sufficient condition for the stochastic convergence of the sample mean $\bar{x}$ to the population mean is that $F \in \Omega_{(1)}$. Hence for all $F \in \Omega_{(1)}$, $\bar{x}$ is a consistent estimate of the population mean; furthermore it is unbiased. If we apply this result to the random variable $Y = X^2$, we find that for all $F \in \Omega_{(2)}$, $\sum_{i=1}^{n} x_i^2/n$ is a consistent unbiased estimate of the second moment of F about the origin. Similar statements may be made for higher moments. For $F \in \Omega_{(2)}$ one may show further that with Q defined as $\sum_{i=1}^{n} (x_i - \bar{x})^2$, the statistics Q/n and $Q/(n-1)$ are consistent estimates of the population variance, and the latter is unbiased.

[10] See, for example, J. L. Doob, *Annals of Math. Stat.*, Vol. 6 (1935), p. 163.

If there exists a number M such that $F(M) = \frac{1}{2}$, it is called the median of the distribution. The median $\tilde{x}$ of a sample of odd size is the central X_i when the X_i are arranged in order of magnitude; for a sample of even size we may take $\tilde{x}$ to be the average of the two central values. It may be shown[11] that $\tilde{x}$ is a consistent estimate of M for F in the subclass of Ω_3 for which the probability density function $f(x)$ is continuous at $x = M$ and $f(M) \neq 0$.

8. Confidence intervals for an unknown median, for the difference of medians. Arrange the sample in rank order and denote the result by $Z_1 \leq Z_2 \leq \cdots \leq Z_n$, where $Z_1, \cdots, Z_n$ is a rearrangement of $X_1, \cdots, X_n$. The joint distribution of the Z_i (or any subset of the Z_i) is well known [49] if $F(x)$ is restricted to Ω_4, which we now assume. From this distribution theory it is easy to show that for any positive integer $k < \frac{1}{2}n$, the probability that the random interval (Z_k, Z_{n-k+1}) cover the unknown population median M is

$$Pr\{Z_k \leq M \leq Z_{n-k+1}\} = 1 - 2I_{\frac{1}{2}}(n - k + 1, k),$$

where

$$I_x(p, q) = \int_0^x t^{p-1}(1 - t)^{q-1}\,dt \Big/ \int_0^1 t^{p-1}(1 - t)^{q-1}\,dt$$

is the incomplete Beta-distribution tabulated by K. Pearson. The practicability of estimating M by means of the above relation in the non-parametric case was noted first by W. R. Thompson [35]. It is not difficult to calculate tables giving, for various sample sizes n, the maximum k for which $Pr\{Z_k \leq M \leq Z_{n-k+1}\} \geq .95$ or .99. This has been done for $n = 6$ to 81 by K. R. Nair [21], who listed the maximum k as well as $n - k + 1$ and $I_{\frac{1}{2}}(n - k + 1, k)$, so that the exact confidence coefficient is available. Nair also gave asymptotic formulas which are very accurate for $n > 81$.

It is clear how confidence intervals for the difference $d = M_2 - M_1$ of the medians of two univariate populations with c.d.f's known only to be in Ω_4 might be obtained by combining two probability statements of the above kind: Let the desired confidence coefficient be $1 - \alpha$, and form confidence intervals of the above type for M_1 and M_2 with confidence coefficient $1 - \frac{1}{2}\alpha$; write them $Pr\{\underline{M}_i \leq M_i \leq \bar{M}_i\} \geq 1 - \frac{1}{2}\alpha$. Then $Pr\{\underline{M}_2 - \bar{M}_1 \leq d \leq \bar{M}_2 - \underline{M}_1\} \geq 1 - \alpha$. Solutions like this which are easily obtained by the combining method in many problems are in general not very efficient.

Some work of Pitman's [27] may be regarded as a solution of the problem of estimating the difference of medians (or other quantiles, or means) of two populations in a case essentially more restricted than the preceding, but more general than the corresponding parametric case in which the distributions are assumed to differ only in location. To describe the nature of Pitman's result,

[11] This follows from the asymptotic distribution of $\tilde{x}$. See, for instance, [49], and combine section 4.53 with Theorem (A), p. 134.

let us revert to the notation introduced at the beginning of section 4, but add to the assumption that F and G are in a known class Ω, the *restrictive assumption* that F and G differ only in location, that is, that $G(x) = F(x - d)$. The problem is the interval estimation of the unknown constant d. Define the random variables $Z_i = Y_i - d$. After noting that the $m_1 + m_2$ random variables $X_1, \cdots, X_{m_1}, Z_1, \cdots, Z_{m_2}$ are all independently distributed with the same c.d.f. F, Pitman was able to apply his results for the problem of two samples to show how functions $\underline{d}$ and $\bar{d}$ of $X_1, \cdots, X_{m_1}, Y_1, \cdots, Y_{m_2}$ could be calculated such that $Pr\{\underline{d} < d < \bar{d}\} \geq 1 - \alpha$ for $\nu = 0$, while for $\nu = 2$ the equality holds. After fitting an incomplete Beta-distribution Pitman found that the resulting approximate confidence intervals coincide with the well known ones employing the t-distribution and based on the assumption that F and G are normal with the same unknown variance.

9. Confidence limits for an unknown distribution function. Consider in an x, y-plane the graph g of the unknown c.d.f., g being the locus of the equation $y = F(x)$, and the possibility of covering g with random regions $\mathfrak{R}(\mathbf{E})$ depending on the sample $\mathbf{E}$. Wald and Wolfowitz [39] have shown how for given n and α it is possible in a large variety of ways to define regions $\mathfrak{R}(\mathbf{E})$ such that $Pr\{\mathfrak{R}(\mathbf{E}) \supset g\}$, the probability that the random region $\mathfrak{R}(\mathbf{E})$ cover the unknown graph g, is $1 - \alpha$ for all $F \in \Omega_2$. Instead of describing their general method we shall limit ourselves to a special case. This is a very neat solution the necessary distribution theory for which was developed earlier by Kolmogoroff [15].

Let $G_n(x)$ be the "empirical distribution function" of the sample: $nG_n(x)$ is the number of $X_i \leq x$. Define the random variable

$$D_n = \sqrt{n} \sup_x | F(x) - G_n(x) |,$$

and let $\Phi_n(\lambda)$ be the c.d.f. of D_n, $\Phi_n(\lambda) = Pr\{D_n \leq \lambda\}$. Kolmogoroff proved that $\Phi_n(\lambda)$ is independent of $F \in \Omega_2$, and that as $n \to \infty$, $\Phi_n(\lambda) \to \Phi(\lambda)$ uniformly in λ, where $\Phi(\lambda)$ is defined by the rapidly converging Dirichlet series

$$\Phi(\lambda) = \sum_{k=-\infty}^{+\infty} (-1)^k \exp(-2k^2\lambda^2).$$

A small table of values of the function $\Phi(\lambda)$ was given by Kolmogoroff [15], and a larger one by Smirnoff [33]. Define $\lambda_{n,\alpha}$ from $\Phi_n(\lambda_{n,\alpha}) = 1 - \alpha$, and λ_α from $\Phi(\lambda_\alpha) = 1 - \alpha$. Values of λ_α for $\alpha = .05, .02, .01, .005, .002, .001$ were listed by Kolmogoroff [16]. Now $1 - \alpha$ is the probability that

$$\sqrt{n} \sup_x | F(x) - G_n(x) | \leq \lambda_{n,\alpha}$$

if $F \in \Omega_2$. The above inequality is equivalent to

$$G_n(x) - \lambda_{n,\alpha}/\sqrt{n} \leq F(x) \leq G_n(x) + \lambda_{n,\alpha}/\sqrt{n} \qquad \text{(all } x\text{)}.$$

If we take as $\mathfrak{R}(\mathbf{E})$ the intersection of the region between the graphs of the functions $G_n(x) \pm \lambda_{n,\alpha}/\sqrt{n}$, with the strip $0 \leq y \leq 1$, we have $Pr\{\mathfrak{R}(\mathbf{E}) \supset g\} =$

$1 - \alpha$. The values of $\lambda_{n,\alpha}$ have not been tabulated, but for practical purposes of determining an unknown c.d.f. one would usually require a large n, and the tabulated values of λ_α could then be used.

With $\Phi_n(\lambda)$ defined as the c.d.f. of D_n for $F \in \Omega_2$, Kolmogoroff has shown further that for $F \in \Omega_0$, $Pr\{D_n \leq \lambda\} \geq \Phi_n(\lambda)$. This gives the beautiful result that the above confidence belt is valid in the most general case where $F \in \Omega_0$, in the sense that for the above defined $\mathfrak{R}(\mathbf{E})$, $Pr\{\mathfrak{R}(\mathbf{E}) \supset g\} \geq 1 - \alpha$.

10. Tolerance limits. An ingenious formulation and solution of a non-parametric estimation problem was given by Wilks [47]. Let us say that an interval (x', x'') covers a proportion π of a population with c.d.f. $F(x)$ if $F(x'') - F(x') = \pi$. In the notation of section 8, Wilks considered the proportion B covered by the interval (Z_k, Z_{n-m+1}) extending from the k-th smallest observation to the m-th largest, $B = F(Z_{n-m+1}) - F(Z_k)$. B is a random variable depending on the sample but is *not* a statistic since it depends also on the unknown c.d.f. $F(x)$. However, Wilks noted that the c.d.f. $G(b)$ of B is independent of $F \in \Omega_4$, in fact, for $0 < b < 1$,

$$G(b) = I_b(n - k - m + 1, k + m),$$

where $I_z(p, q)$ is defined in section 8. After k, m, a fixed proportion b, and a confidence coefficient $1 - \alpha$ have been chosen, the equation $G(b) = \alpha$ determines the sample size n for which we can then make the following assertion without any knowledge of F except that $F \in \Omega_4$: The probability is $1 - \alpha$ that in a sample size n the random interval (Z_k, Z_{n-m+1}) will cover at least $100\ b\%$ of the population.[12]

Wilks considered, among other extensions of his method, tolerance limits for multivariate distributions in which the variables are known to be independent, and the estimation of proportions in a second sample (instead of in the population) on the basis of a first sample [48]. The latter problem involves the calculation of $P(b; n, N, k, m)$, the probability that if a first sample of n is taken and then a second sample of N, a proportion b or more of the second sample will lie in the interval (Z_k, Z_{n-m+1}) determined from the first sample. Wilks' derivation of P requires the assumption that $F \in \Omega_4$, but a simple auxiliary argument (related to the method of randomization by ranks) will extend the validity to the case $F \in \Omega_2$: The complete set of $n + N$ variates is independently distributed, each with the same c.d.f. $F \in \Omega_2$. All $(n + N)!$ possible rankings (excluding the "tied" ranking R_0) as defined in section 2 then have the same probability $1/(n + N)!$. The fraction of these rankings for which the statement about proportions in the second sample is correct is a function of b, n, N, k, m only, and not of $F \in \Omega_2$, and this fraction is the desired P. Since P is the same for all $F \in \Omega_2$ it must of course coincide with the value calculated by Wilks for $F \in \Omega_4$. It would be desirable for practical purposes to extend the validity of the tolerance

[12] For fixed b, $G(b)$ of course takes on discrete values with n, so one would either choose the n giving $G(b)$ the nearest value to α or else the greatest value $\leq \alpha$.

limits of the first paragraph, concerning proportions in the population, at least to the case $F \in \Omega_3$. The extension to Ω_2 would follow immediately if the intuitively reasonable statement $1 - G(b) = \lim_{N\to\infty} P(b; n, N, k, m)$ could be justified for $F \in \Omega_2$.

The multivariate case when independence is not assumed was successfully attacked by Wald [38]. We shall describe here his solution for the bivariate case: Let (X_i, Y_i), $i = 1, \cdots, n$, be a sample from a population with bivariate c.d.f. $F(x, y) \in \Omega_4^{(2)}$, that is, F is of the form

$$F(x, y) = \int_{-\infty}^{x}\int_{-\infty}^{y} f(\xi, \eta)\, d\eta\, d\xi,$$

where $f(x, y)$ is continuous, but otherwise unknown. Plot the points (X_i, Y_i) in an x, y-plane and choose four (small) integers k_1, m_1, k_2, m_2. . Draw vertical lines (parallel to the y-axis) passing through the points with the k_1-th smallest and m_1-th largest abscissas. Considering *only* the $n - k_1 - m_1$ points inside these vertical lines (the probability of equal abscissas is zero), draw two horizontal lines passing through the points with k_2-th smallest and m_2-th largest ordinates. Let J be the rectangle bounded by the four lines and consider the proportion B of the population covered by the rectangle, $B = \int_J dF(x, y)$. Then the c.d.f. $G(b)$ of B is given by the previous formula in terms of the incomplete Beta-distribution with $k + m = k_1 + k_2 + m_1 + m_2$, and is thus independent of $f(x, y)$. Choose k_1, k_2, m_1, m_2, b, and α. Then the equation $G(b) = \alpha$ determines the sample size n for which the probability is $1 - \alpha$ that the random rectangle J will cover at least 100 $b\%$ of the population. Wald showed further how a series of rectangles instead of a single rectangle might advantageously be used in the case of highly correlated X, Y.

It would be most useful to have tables of n corresponding to $\alpha = .05$ and .01, some values of b close to unity, and a few small values of $k + m$, say, $k + m = 2, 4, \cdots, 2r$. The table could then be used for the univariate, bivariate, $\cdots$, r-variate cases with various choices of k_j, m_j, such that $\Sigma(k_j + m_j) = k + m$. Entries for $k + m = 4$ have been given by Wald [38, p. 55].

Part III. Toward a General Theory

11. The criterion of consistency. All the concepts of Part III have been carried over from, or suggested by, corresponding ones earlier developed for the parametric theory. Consistency of point estimation was defined in section 7. Wald and Wolfowitz [40] have generalized the notion of consistency to tests so that it is applicable in the non-parametric case. We have heretofore specified the hypothesis H and its admissible alternatives by means of classes of n-variate c.d.f's F_n. We now assume that H and its admissible alternatives can be framed as statements about one or more populations, independent of n. Thus in the problem of two samples (section 4) H may be taken as the statement that the c.d.f's F and G of the two populations are the same member of Ω_r, while the

admissible alternatives are statements that F and G are any two different members of Ω_r. Returning to the general case, we assume that a sequence of tests is under consideration, say, $\mathfrak{T}_1, \mathfrak{T}_2, \cdots$, such that as $j \to \infty$, the size of the sample in $\mathfrak{T}_j$ from each of the populations becomes infinite. The sequence $\{\mathfrak{T}_j\}$ may be called simply a "test" and is said to be consistent if the probability of rejection of H by $\mathfrak{T}_j$ approaches unity as $j \to \infty$ whenever an admissible alternative to H is true. It has been suggested [50] that consistency is a minimal requirement for a good test. In order to allow for the analogue of the "common best critical regions" in the parametric theory,[13] it would be better to define consistency with respect to any given subset of the admissible alternatives and then require consistency with respect to the subset appropriate to the specific situation in which the test is to be used.

Wald and Wolfowitz [40] proved that under certain restrictions on the admissible F, G in the problem of two samples their test based on runs (section 4) is consistent, while another previously proposed test is not. Judging from their work, we may expect that, while inconsistency proofs may be easy, consistency proofs will be difficult.

12. Likelihood ratio tests. A definition of the Neyman-Pearson likelihood ratio criterion[14] λ for testing the hypothesis H (we use the notation of section 2), which would yield the usual result in the parametric case, would be the following: Let $C(E;\delta)$ be a cube of edge 2δ in the sample space W with center at the point E and faces parallel to the coordinate hyperplanes, and let $P(E;\delta \mid F_n)$ be the "probability put into the cube by the c.d.f. F_n", that is, $P(E;\delta \mid F_n) = \int_{C(E;\delta)} dF_n$. Define

$$\lambda(E;\delta) = [\sup_{F_n \in \omega} P(E;\delta \mid F_n)]/[\sup_{F_n \in \Omega} P(E;\delta \mid F_n)],$$

$$\lambda = \lambda(E) = \lim_{\delta \to 0} \lambda(E;\delta).$$

This definition of λ is not useful in the non-parametric case as λ turns out in general to be independent of E; the reader may easily verify this for the problem of two samples (section 4).

Having seen now that the likelihood ratio does not carry over to the non-parametric case in an obvious way, we are in a position to appreciate a bold stroke by Wolfowitz [50]. He begins by limiting the critical regions to be considered to the relatively small class obtainable by the method of ranks (section 2). Let $R = R(\mathbf{E})$ be the ranking of the sample point $\mathbf{E}$, so that the random variable R takes on the possible values $R_0, R_1, \cdots, R_s$, and let $P(R_\sigma \mid F_n) = Pr\{R = R_\sigma \mid F_n\}$.

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[13] J. Neyman and E. S. Pearson, "On the problem of the most efficient tests of statistical hypotheses", *Phil. Trans. Roy. Soc. London*, A, Vol. 231 (1933), pp. 289–337.

[14] J. Neyman and E. S. Pearson, *Biometrika*, Vol. 20A (1928), p. 264.

Then Wolfowitz takes the likelihood ratio to be the following function of the ranking R:

$$\Lambda(R) = [\sup_{F_n \in \omega} P(R \mid F_n)]/[\sup_{F_n \in \Omega} P(R \mid F_n)].$$

His modified likelihood ratio test then consists of applying the method of ranks (section 2) with $\Lambda(R)$ as the statistic, small values being regarded as significant. If Ω is a class of continuous F_n, all rankings $R \neq R_0$ have the same probability $1/s$ under the null hypothesis, while $P(R_0 \mid F_n) = 0$ for all $F_n \in \Omega$. Then the numerator of $\Lambda(R)$ is $1/s$, and we may thus use the denominator of $\Lambda(R)$ as statistic with large values significant. Wolfowitz' modification has one advantage we don't always find with the usual parametric method: it always leads to similar regions since it is a special case of the randomization method.

In applying his method to examples Wolfowitz finds it necessary to resort each time to an approximation in calculating his statistic $\Lambda(R)$. Instead of taking the "sup" over Ω as in the definition, he takes it instead over a subclass Ω' of Ω which lends itself more easily to calculation. Thus in the problem of two samples with $\nu = 2$, whereas Ω is the class defined in section 4 with F, G in Ω_2, the class Ω' is the subclass of Ω obtained by further limiting F, G as follows: The x-axis is divided up into a number of disjoint intervals, equal to the total number of runs in the sequence V defined in connection with the Wald-Wolfowitz test in section 4. If the j-th run in V is a run of 1's the restriction $G(x) = 0$ in the j-th interval is imposed, if the j-th run is a run of 2's, $F(x) = 0$ in the j-th interval. The intervals in which F, G are permitted to assign positive probability then correspond in order and number to the two kinds of runs. With this restriction the (twice) modified likelihood ratio statistic is found to be

$$\sum_i \sum_j (l_{ij} \log l_{ij} - \log l_{ij}!),$$

where l_{ij} is the number of elements in the j-th run of i's ($i = 1, 2$). Large values are significant. For large samples the asymptotic distribution of the statistic falls out as a special case of a general theorem of Wolfowitz.

In the same paper Wolfowitz obtained modified likelihood ratio tests for the problem of k samples and the problem of independence of two or more random variables.

In his examples the author states that the maximizing F_n in Ω' is "essentially the same" as the maximizing F_n in Ω, at least for the significant rankings R_σ and for large samples. The necessity of this approximation procedure is somewhat disturbing, as is the restriction to the method of ranks. Since it does not seem possible to give a definition of likelihood ratio tests sufficiently broad to include the non-parametric case, yet yielding the usual result in the parametric case, we are denied even the small comfort of saying that at least in special cases the method is known to yield optimum results. In some problems the set $\{R_\sigma\}$ of rankings, corresponding to the set $\{w_\sigma\}$ of regions in W which serves to separate the s points of the subpopulations $\{E'\}$ defined in section 2, is not

unique—consider for instance the problem of two samples when the populations are bivariate—and in such cases the method as defined above would not give a unique result. These remarks are intended to point the need for further investigation and cannot detract from the ingenuity of the method—the first general process that has been suggested for choosing one out of the welter of similar regions yielded by the randomization method.

13. Wald's formulation of the general problem of statistical inference. A formulation of the general problem of statistical inference broad enough to cover the non-parametric case, and including estimation and tests as well as statistical problems classifiable under neither of these headings, has been given by Wald [37]. This formulation extends certain concepts he had applied earlier[15] to the parametric case.

In this last section we shall permit ourselves a somewhat more abstract terminology and notation than before. As in section 2, $\mathbf{E} = (X_1, \cdots, X_n)$ will denote the sample; $F_n(E)$, its c.d.f.; W, the n-dimensional Euclidean space of E, the sample space; and Ω, the space of admissible F_n. Of central importance is a given class $\mathfrak{S}$ appropriate to the problem, $\mathfrak{S} = \{\omega_\beta\}$, whose members ω_β are (not necessarily disjoint) subsets of Ω, $\Omega = \bigcup_\beta \omega_\beta$. To every $\omega_\beta \in \mathfrak{S}$ there corresponds a hypothesis $H(\omega_\beta): F_n \in \omega_\beta$, so that there is a 1:1 correspondence between the members of the set $\mathfrak{S}$ and those of the set $\{H(\omega_\beta)\}$ of hypotheses. The general problem of statistical inference, according to Wald, is the choice of a decision function $\Delta(E)$ mapping W into $\mathfrak{S}$. For every $E \in W$ a decision function $\Delta(E)$ uniquely selects an element ω_β of $\mathfrak{S}$, $\omega_\beta = \Delta(E)$. Its statistical import is that when the sample point $\mathbf{E}$ equals E, we agree to accept the hypothesis $H(\omega_\beta)$ determined by $\Delta(E) = \omega_\beta$.

Before introducing any further definitions let us illustrate the preceding ones. In any problem of testing a hypothesis, the set $\mathfrak{S}$ has just two members ω_1 and ω_2 which we have heretofore denoted by ω and $\Omega - \omega$, respectively. The decision function $\Delta(E)$ then takes on just these two values, in fact, $\Delta(E) = \omega_2$ for E in the critical region w of the test, and $\Delta(E) = \omega_1$ for $E \in W - w$.

To illustrate the definitions in the case of point estimation, consider estimating the median M of a univariate population with c.d.f. $F(x)$. Ω would be the class of F_n of the form $\prod_{i=1}^n F(x_i)$ with, say, $F \in \Omega_4$ and $F'(M) \neq 0$ (which is sufficient to insure a unique M). The index β could now be identified with M, so that its domain is the real line, and $\omega_\beta = \{F_n \mid M(F) = \beta\}$. The classes ω_β would be disjoint in this case and each would contain an infinite number of F_n. The problem of estimating the unknown M may be said to be the choice of a decision function $\Delta(E)$: When $\mathbf{E} = E$ we accept $H(\omega_\beta): F_n \in \omega_\beta = \Delta(E)$, meaning in this case simply that we accept the statement that M equals the β determined by $\Delta(E)$.

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[15] A. Wald, "Contributions to the theory of statistical estimation and testing hypotheses", *Annals of Math. Stat.*, Vol. 10 (1939), pp. 299–326.

Suppose next that instead of the point estimation of M just discussed we are interested in the interval estimation of M. We define Ω as above, and now take the index β to consist of a pair a, b of real numbers. An interval estimate $a \leq M \leq b$ may be regarded as an acceptance of the hypothesis $H(\omega_{a,b}): F_n \in \omega_{a,b}$, where $\omega_{a,b}$ is the subclass of Ω consisting of all F_n for which $M(F)$ lies in the interval $a \leq M \leq b$. The set $\mathfrak{S}$ now consists of all classes $\omega_{a,b}$ with $-\infty < a < b < +\infty$. Here as in the general case of interval estimation the classes ω_β of the set $\mathfrak{S}$ are not disjoint. The decision function $\Delta(E)$ adopted in section 8 is $\Delta(E) = \omega_{a,b}$ with $a = z_k$, $b = z_{n-k+1}$, where $z_1 \leq z_2 \leq \cdots \leq z_n$ is a rearrangement of the coordinates $x_1, \cdots, x_n$ of E.

An example of a problem neither of estimation nor testing would be the following: Let Ω be as above. Two real numbers A and B $(A < B)$ are given and it is required to decide on the basis of the sample $\mathbf{E}$ to which of the three classes $-\infty < M < A, A \leq M \leq B, B < M < +\infty$ the unknown median M belongs. Here the set $\mathfrak{S}$ would consist of three disjoint classes $\omega_1, \omega_2, \omega_3$: where ω_1 is the subclass of Ω consisting of F_n with $M(F) < A$, etc.

We return now to the general case. Before defining a "best" decision function $\Delta = \Delta^*$, Wald asks that there be a given weight function $w(F_n, \omega_\beta)$ defined on the product space $\Omega \times \mathfrak{S}$. The weight function $w(F_n, \omega_\beta)$ is a real-valued function evaluating the loss involved in accepting $H(\omega_\beta)$, the statement that the unknown c.d.f. of $\mathbf{E}$ is a member of ω_β, when the unknown c.d.f. is actually F_n. If $F_n \in \omega_\beta$ we make no error in accepting $H(\omega_\beta)$, and in this case w is defined to be zero. Its value otherwise is required to be non-negative. In this theory the choice of the weight function is regarded as essentially *not* a mathematical problem, but the choice is to stem out of the very specific situation in which the statistical inference is to be made. In an industrial problem w might be the financial loss incurred when a certain kind of error is made.

After w is given, the decision functions Δ are to be restricted to the class for which $w(F_n, \Delta(E))$ is a Borel-measurable function of E for all $F_n \in \Omega$; note that w depends on E only through Δ, not through F_n. The expected value of w for a particular F_n is called the risk function; it depends of course on the decision function Δ and the weight function w as well as on F_n. Denote it by

$$r(\Delta, w \mid F_n) = \int_W w(F_n, \Delta(E))\, dF_n(E).$$

Since the true F_n is unknown, so in general will be the true value of the risk function associated with a particular decision function Δ. We might call

$$r(\Delta, w) = \sup_{F_n \in \Omega} r(\Delta, w \mid F_n)$$

the maximum risk associated with the decision function Δ. Wald defines Δ^* to be the "best" decision function relative to the weight function w if the maximum risk $r(\Delta, w)$ is minimum for $\Delta = \Delta^*$. He points out that the "best" decision

function might be defined as one which minimizes some weighted mean, taken over all $F_n \in \Omega$, of the risk function $r(\Delta, w \mid F_n)$, but that the above definition of the "best" decision function has certain advantages. Thus under certain restrictions on Ω and w, the risk function $r(\Delta^*, w \mid F_n)$ is independent of $F_n \in \Omega$, that is, we then know the exact value of the risk, regardless of what the true F_n may be. This is analogous to the desirable situations where confidence intervals are known, and the probability of a false statement (to the effect that the unknown quantity is in a given region when it is not) is then a constant independent of the unknown quantity.

Wald's theory is suggestive and formally very satisfying, but one would like to see some specific examples of its application to non-parametric cases. A discouraging aspect, not shared by the older Neyman-Pearson theory, lies in the very refinement that a decision function is declared best with respect to a very particular weight function w. An attractive possibility would be to impose a metric on Ω or on a related function space, and to let w be the distance function. In the problem of two samples for example, after metrizing Ω_2, the weight w assigned to accepting H might be taken as the distance between F and G in the notation of section 4. A suitable choice of metric might yield a weight function appropriate to a large variety of situations. The difficulties of finding a distance function which is intuitively satisfactory and analytically tractable in calculating the risk function are no doubt formidable. The device of metrizing a space of distribution functions was used by Mann and Wald in a different connection [17], but their choice of distance function, while appropriate to their problem, would not be satisfactory here.

Also still lacking is any general theory relating the three concepts discussed in Part III. The following questions have been answered, at least for some specific examples, in the parametric case, but are still untouched in the non-parametric case: Are likelihood ratio tests consistent? Is there a simple weight function w relative to which the likelihood ratio test becomes a "best" test, or asymptotically a "best" test? If a test is "best" relative to a given weight function, with respect to what set of alternatives is it consistent?

In conclusion let us emphasize the need for *constructive* methods of obtaining "good" and "best" tests and estimates in the non-parametric case. Recalling the history of the parametric case we may judge that half the battle was the definition of "good" and "best" statistical inference. Progress in the non-parametric case has been made in the direction of definition, mainly by carrying over or modifying criteria originally advanced for the parametric case. However, besides criteria for "good" and "best" tests and estimates, we have in the parametric case a large body of constructive theory which may be applied in particular examples to yield the optimum tests or estimates; thus we have the Fisher theory of maximum likelihood statistics for point estimation, and the constructive theorems of the Neyman-Pearson theory for the existence of critical regions of types A, A_1, B, B_1, and the related types of "best" confidence inter-

vals. The contrasting lack of any general constructive methods[16] at present challenges us in the non-parametric theory.

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ON THE THEORY OF SAMPLING FROM FINITE POPULATIONS

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I—HISTORICAL BASIS FOR MODERN SAMPLING THEORY

The theory for independent random sampling of elements from a population where the unit of sampling and the unit of analysis coincide was developed by Bernoulli more than 200 years ago. The theory that would measure the gains to be had from introducing stratification into sampling was indicated by Poisson a century later. Subsequently, Lexis systematized previous work and provided the theoretical basis for sampling clusters of elements.[1] The adaptation of the work of Bernoulli and Poisson to sampling from finite populations was summarized by Bowley in 1926 [1] approximately a century after the work of Poisson.

An impetus to sampling advancement, following some fundamental statistical contributions of Pearson, Fisher, and others, resulted from the work of Neyman when he published his paper in 1934 on the two different aspects of the representative method [8]. In that paper he introduced new criteria of the optimum use of resources in sampling, including the concept of optimum allocation of sampling units to different strata subject to the restriction that the sample have a fixed total number of sampling units.

If, no matter how a sample be drawn, the cost were dependent entirely on the number of elements included in the sample, there would be little need for theory beyond the classical theories of Bernoulli and Poisson covering the independent random sampling of elements within strata, supplemented by the extension of the theory to finite populations, and the extension to optimum allocation of sampling units. Very often, however, in statistical investigations it is extremely costly, if not impossible, to carry out a plan of independent random sampling of elements in a population. Such sampling, in practice, requires that a listing identifying all the elements of the population be available, and frequently this listing does not exist or is too expensive to get. Even if such a listing is available, the enumeration costs may be excessive if the sample is too widespread. Frequently also, there are other restrictions on the sample design, such as the requirement that enumerators work under the close supervision of a limited number of supervisors, and as a consequence the field operations must be confined to a limited number of administrative centers. Techniques such as cluster sampling [2, 3, 4, 5, 6, 7, 8, 10], subsampling, and double sampling [9], have been

[1] The sampling of clusters of elements refers to the sampling of units that contain more than one element. Examples of cluster sampling include the use of the city block or the county as the sampling unit when the purpose of the survey is to determine the properties of the population made up of individual persons or individual households. In these instances, the city block or county is referred to as the cluster of elements, and the individual person or household is referred to as the element.

developed with the aim of making most effective use of available resources, while keeping within existing administrative restrictions, and thus producing the maximum amount of information possible within these resources and restrictions. Neyman [8], Yates and Zacopanay [10], Cochran [2], Mahalanobis [7], and others have made important contributions in this regard.

We can illustrate a number of the developments indicated above in a simple but fairly general subsampling design. This design involves the sampling of clusters of elements from a stratified population and the subsampling of elements from each of the selected clusters, where the number of elements in each of the primary sampling units within a stratum is the same.

Suppose we have a population made up of L strata, with the i-th stratum containing M_i primary sampling units of N_i elements each. The individual element will be the subsampling unit. Let X_{ijk} be the value of some characteristic of the k-th element of the j-th primary sampling unit in the i-th stratum, and assume that the character to be estimated is

$$\bar{X} = \sum_{i}^{L} \sum_{j}^{M_i} \sum_{k}^{N_i} X_{ijk} \Big/ \sum_{i}^{L} M_i N_i . \tag{1}$$

For example, if $\bar{X}$ is the average income per household in a given city, X_{ijk} might be the income of the k-th household in the j-th city block in the i-th ward; where the household is the subsampling unit, the city block is the primary sampling unit, and the stratification has been by wards. Suppose, further, that we sample m_i primary units from the i-th stratum, and subsample n_i elements from each of the primary units sampled from that stratum.

The "best linear unbiased estimate" [8] of $\bar{X}$ from the sample will be

$$\bar{X}' = \sum_{i}^{L} \frac{M_i N_i}{m_i n_i} \sum_{j}^{m_i} \sum_{k}^{n_i} X_{ijk} \Big/ \sum_{i}^{L} M_i N_i , \tag{2}$$

and the variance of $\bar{X}'$ is

$$\sigma^2_{\bar{X}'} = \sum_{i}^{L} M_i^2 N_i^2 \left\{ \frac{M_i - m_i}{M_i - 1} \frac{\sum_{j}^{M_i} (\bar{X}_{ij} - \bar{X}_i)^2}{M_i m_i} + \frac{N_i n_i}{N_i - 1} \frac{\sum_{j}^{M_i} \sum_{k}^{N_i} (X_{ijk} - \bar{X}_{ij})^2}{M_i N_i m_i n_i} \right\} \Big/ \left(\sum_{i}^{L} M_i N_i \right)^2 \tag{3}$$

where $\bar{X}_{ij} = \sum_{k}^{N_i} X_{ijk}/N_i$ and $\bar{X}_i = \sum_{j}^{M_i} \sum_{k}^{N_i} X_{ijk}/M_i N_i$.

These formulas have no practical utility in designing samples unless there are, in addition, some considerations of differential costs. Cost relationships sometimes may be stated explicitly as a function of the m_i and the n_i, or, what is frequently the case, they may be approximated sufficiently through intuition and speculation to guide one to a reasonable decision among the various alternatives implied by the design.

If we know the cost function we proceed to determine the values of the m_i and the n_i that make $\sigma^2_{\bar{x}'}$ a minimum for a fixed total expenditure, and also subject to any other restrictions that may be imposed. This theory provides a basis for determining the optimum allocation of the sampling ratios to the various strata, and to primary and secondary sampling units within each stratum.

Such developments, however, must be regarded as only the first step in sample design. We cannot go forward if we only know that the optimum sample design is some particular mathematical function of the population parameters and the cost factors; we need also to know something about the relative magnitudes of certain parameters in the particular populations under consideration, as well as something about the costs associated with the various sampling and estimating operations.

Thus, considerable work in recent years has been done on the study of the relative magnitudes of variances and covariances between and within various types of sampling units and on the study of costs and types of cost functions that operate. Work is being done in this field by the Department of Agriculture in connection with sampling for agricultural items, and is being done also in the Bureau of the Census, and in other places.

II—THE DIRECTION OF MORE RECENT DEVELOPMENTS

The sampling procedure indicated above involves as a first step the definition of the *system of sampling*, such as whether the sampling method will involve cluster sampling, double sampling, or subsampling, and along with this the definition of the stratification and the sampling units. The second step is that of determining the *method of estimation*, together with *the allocation of the sampling units.*

The first step, that of defining the sampling system is taken with a view to administrative feasibility and sampling efficiency, but no simple procedure exists which leads one uniquely to the selection of a system except perhaps by the impractical method of listing and examining all possible alternatives and accepting one on some criterion of best. However, given the definition of a population character to be estimated, and a sampling system, a simple procedure is available that will provide a unique solution to the second step providing we accept some criterion as to what "best" means, such as the best linear unbiased estimate, subject to any cost or administrative restrictions that may be imposed. Such criteria lead us to both our estimating procedure and our allocation of sampling within the sampling system defined.

While no theory with practical applicability has been developed which indicates a "best" system of sampling, and at the same time indicates the "best" estimating procedure and sampling allocation, some progress in the choice of improved sampling systems and estimating procedures has been made. The developments in the following two directions appear to us to be particularly pertinent.

1. Modifications in some of the fairly generally accepted criteria of good

sample estimates have led to more reliable sample results for some types of sampling systems (some of these are mentioned in Sec. III);

2. Some principles are emerging, that have led to improved determination of the sampling units, the strata, and other aspects of the sampling system (some efforts at formulating such principles are reported in Secs. IV, V, and VI).

We shall summarize, principally, some of the recent work in the Census—and in so doing shall mention some work of others that is closely related. Most of the work that we shall summarize relates to problems where the sampling units are clusters of elements and vary in size.

III—MODIFICATIONS IN THE CRITERIA FOR GOOD ESTIMATES

The estimate given in the general subsampling problem formulated in Sec. I satisfies the criterion of the "best linear unbiased estimate." Also, as far as our experience has indicated, this estimate is frequently the most efficient one for populations of the form described, that is, where the number of elements in each sampling unit within a stratum is the same. However, if the numbers of elements differ between sampling units, a biased but consistent estimate can frequently be found that has a substantially smaller mean square error[2] than the best linear unbiased estimate.

For example, consider the case where clusters of elements are the sampling units and we want to estimate $\bar{X} = \sum_i^M X_i / \sum_i^M N_i$, the average value per element of some specified characteristic. Here M is the number of sampling units in the population, X_i is the aggregate value of the specified character for all elements in the i-th cluster, and N_i is the number of elements in that cluster. The joint distribution of X_i and N_i is unknown, but $\sum_i^M N_i = N$ is known. Under these circumstances the "best linear unbiased estimate" of $\bar{X}$ from a sample of m clusters turns out to be $\frac{M}{m} \sum_i^m X_i / N$. However, a smaller mean square error is often obtained by the use of a ratio estimate from the sample such as $\sum_i^m X_i / \sum_i^m N_i$. This estimate is excluded by the "best linear unbiased" criterion because it is nonlinear and biased, although the bias is usually negligible and the estimate is consistent. Since the best linear unbiased estimate of $\bar{X}$ requires the knowledge of N, the sample ratio has a further advantage in that it can be used even when N is not known.

A recent paper by Cochran [3] gives a number of consistent though biased esti-

[2] In this paper the terms "mean square error" and "variance" are used interchangeably to refer to $E(X - \hat{X})^2$ when EX is equal to $\hat{X}$, the population character to be estimated. When EX is not equal to $\hat{X}$, however, $E(X - \hat{X})^2$ will be referred to only as the "mean square error." Since, under these latter circumstances, $E(X - \hat{X})^2 = E(X - EX)^2 + (EX - \hat{X})^2$, the mean square error is equal to the variance of X plus the contribution due to the bias.

mates of $\bar{X}$ that make use of the least square estimate of the linear regression of X_i on N_i. These estimates generally have a smaller mean square error than either the best unbiased linear estimate or the simple ratio estimate given above. However, they require knowledge of N, as does the best linear unbiased estimate, and in addition may require detailed tabulations and considerable clerical work as a part of the estimating process.

Both types of biased estimates mentioned above are consistent, and usually have a smaller mean square error than the best linear unbiased estimate for sampling systems in which the sampling units vary in size. Thus, improved sample estimates will be obtained by modifying the "best linear unbiased estimate" criterion to include estimates that are nonlinear, consistent, but have a smaller mean square error than the best linear unbiased estimate.

IV—IMPROVEMENTS IN THE SPECIFICATIONS OF SAMPLING SYSTEMS

A great deal can be done to improve sampling designs through improved specification of the sampling system even though one has only a limited knowledge of the manner in which the population is likely to be made up, and no specific information concerning the particular population parameters involved (see Sec. VI).

1. The sizes of sampling units. A number of recent investigations have indicated the desirability, with costs considered, of keeping the size of cluster very small when clusters of elements are used as the sampling unit in field surveys [2, 5, 6, 7, 8]. It is important to point out, however, that this principle is not necessarily applicable to subsampling systems, and that the use of large clusters as the primary sampling units in a system involving subsampling may yield distinct gains over the use of smaller clusters without subsampling. Moreover, one of the often recurring problems in large-scale studies is the designing of sample surveys within stringent administrative restrictions on the number of different locations in which operations can be carried on. Under such restrictions a procedure commonly used is to choose a limited number of existing political units, such as counties, as the primary sampling units, and then to subsample units such as blocks, small rural areas, or households. Under the circumstances, if the numbers of primary subsampling units to be included in the sample are assumed to be held constant, the use of larger primary sampling units than the existing political units would have the effect of decreasing the sampling variance.

The advantage of using large primary units in subsampling is evident in the simple case when the original units, each having the same number of elements, are consolidated to form half as many enlarged primary units, each twice as large as the original units. The variance between the enlarged primary units will be $\sigma^2_{2b} = \frac{1}{2}\sigma^2_{1b}(1 + \rho)$, where σ^2_{1b} is the variance between the original primary units, and ρ is the correlation between the units that are paired. The correlation coeffi-

cient will be close to zero (exactly equal to $-1/\{M-1\}$, where M is the number of original primary units) if the pairing is done at random, and it follows that the variance between counties is then cut at least in half. Ordinarily, ρ will be greater than zero if the paired units are required to be contiguous. However, through choosing for consolidation those contiguous units that are as different as possible, ρ is made as small as possible, and in some instances this minimum value may even be negative. In any event, the smaller the value that ρ takes on, the greater the reduction of the sampling variance between primary units from the use of enlarged units. While the sampling variance within primary units is increased by such consolidations, the increase is slight, and the total sampling variance is almost invariably decreased (see Appendix, Section 1).

The restriction on extending the consolidation of primary units is introduced by the increased cost of subsampling within larger and larger areas. This increased cost is to be weighed against the decreased variance. If the cost restriction were not sufficiently severe, consolidation would proceed to the point of eliminating the use of primary sampling units altogether, and the subsampling units would be selected independently throughout the entire stratum.

2. Subsampling where the primary units are of unequal size. Use of probability proportionate to size in subsampling. A subsampling system frequently followed, whether or not the primary sampling units vary in size, involves the selection of one or more primary units from each stratum with the probability of selection the same for each primary unit in the stratum, and the subsampling of a fixed proportion of the subsampling units from the selected primary unit. When the primary units vary in size this subsampling system has some administrative disadvantages that arise because the number of subsampling units to be included in the sample will vary with the number of elements in the selected primary unit. (The term "size" of sampling unit as used in this paper refers to the number of elements in the sampling unit.)

The disadvantages in the above system have led in some instances to the specification of a second subsampling system in which, although the primary units were selected with equal probability, the subsampling has been of a constant *number* rather than of a constant proportion.

A third subsampling system that can be recommended over both the above systems is to make the probability of selection of a primary unit proportionate to its size and then to subsample a constant number of subsampling units.

We shall assume that for all three systems only one primary unit is selected from each stratum. Stratification to this degree leads to a smaller sampling variance than does less extensive stratification. For simplicity in making comparisons, we shall assume, furthermore, that the subsampling unit is the element of analysis and that the sample estimate used is of the form $\bar{X}' = \Sigma N_h \bar{X}'_h / \Sigma N_h$ where $\bar{X}'_h$ is the sample average, for the h-th stratum, of the character being estimated, and N_h is the size of that stratum. This estimate, which is frequently used, is biased for the first two systems but unbiased for the recommended sys-

tem. However, an unbiased estimate, say the "best" linear unbiased estimate for the first two systems generally has a much larger mean square error than the biased estimates used in these comparisons and hence has not been considered in the comparisons which follow (see Sec. VII, footnote 7).

The first two subsampling systems mentioned are about equally efficient when the number of subsampling units drawn from each primary unit is reasonably large, but each will usually have a larger mean square error than will the recommended system. The difference between the mean square errors of either of the first two and that of the recommended design is given approximately by

$$(4) \qquad \frac{1}{N^2} \sum_h Q_h \bar{N}_h \sigma_h^2 \left[\sum_j \rho_{hj} \bar{N}_h - \sum_j \rho_{hj} N_{hj} \right]$$

where, within the h-th stratum, N_{hj} is the number of elements in the j-th primary sampling unit, $\bar{N}_h$ is the average size of primary sampling unit, Q_h is the number of primary sampling units, ρ_{hj} is the intra-class correlation between elements within the j-th unit and σ_h^2 is the variance between individual elements within the stratum; L is the number of strata. (See Section 2 of the Appendix for the development of this difference.)

This difference, which is a multiple of the average covariance between the N_{hj} and ρ_{hj}, will be positive if N_{hj} and ρ_{hj} are negatively correlated, and this is exactly the situation that exists in most practical problems we have encountered in sampling for social and economic statistics (see Sec. VI).

The reduction in the mean square error arises because the recommended design provides a more nearly optimum allocation of sampling as between large and small sampling units than do the other two. It might be possible, of course, as another alternative, to stratify the primary units by size and then allocate sampling to the various strata on the basis of optimum sampling considerations. However, this would mean that some other and perhaps more important modes of stratification would be sacrificed, and moreover, the optimum allocation of sampling between the larger and smaller units could only be guessed at in most practical problems. Furthermore, it usually is not possible to stratify on size to the point that there is no variation in the sizes of units within a stratum.

The sample estimate from the recommended system is unbiased whereas the estimates from the other two are usually biased, and sometimes fairly seriously so. (For a proof of this statement see Appendix, Section 1, and see also Sec. VII for a numerical illustration.)

The use of probability proportionate to size serves to decrease only the sampling variation between primary units and has very little effect on the sampling variance within. Therefore, the recommended design shows its greatest advantage over the two alternatives when the contribution of the mean square error between primary units to the total mean square error is large.

Ordinarily, the actual sizes of the primary sampling units will not be known, but numbers may be known that are highly correlated with the sizes. For example, ordinarily we will not know the populations of blocks or of cities or

counties at the time a sample is taken, but we may know their populations at the preceding census. Under these circumstances the primary units may be sampled with probabilities proportionate to the previously known (or their estimated) sizes, but if this is done the subsampling is to be modified in order to take account of the changes in the sizes between the two dates. If the actual sizes are known, the constant number taken from the selected primary unit in the h-th stratum is $n_h = t_h N_h$ where t_h is the sampling ratio assigned to the stratum, and N_h is the total number of elements in the stratum. The subsampling ratio within the selected primary unit, therefore, is $t_h N_h / N_{hj}$, where N_{hj} is the number of elements in the selected unit. On the other hand, if there is available only a measure of size P_{hj} highly correlated with the actual sizes of the units N_{hj} and, if the probability of selection of the primary unit has been proportionate to the P_{hj} the subsampling ratio in the selected primary unit will be equal to $t_h P_h / P_{hj}$, where P_h is the measure of size of the entire stratum, and P_{hj} is the measure of size of the selected primary unit. The variance of a sample estimate where measures of size are used is given subsequently in this paper (see Eq. (9)).

3. The use of area substratification within primary strata in a subsampling system. Another modification, which will be called area substratification within primary strata, may be particularly useful where a relatively small sample is required from a population covering a large area, and where operations must be confined to a limited number of centers.

Some preliminary remarks are necessary before area substratification can be explained. Area substratification requires (a) that the entire population to be sampled be divided into areas that will serve as primary sampling units; (b) that these units be further subdivided into a number of sub-areas; and (c) that certain summary statistical information be available for each of the sub-areas in advance of drawing the sample. The information that must be known for the sub-areas includes a reasonably good measure of their sizes (perhaps the total population, total dwelling units, or total farms) and other information which is indicative of the characteristics of the area, such as whether predominantly farm or nonfarm, predominantly white or colored, etc. The sub-areas, when grouped into homogeneous classes, will serve only to determine the substrata described subsequently, and will not ordinarily serve as the subsampling units, which may be defined independent of the sub-areas.

The definition of the primary sampling units and the classification of them into strata proceed as indicated earlier, with the primary units made as internally heterogeneous as possible within strata that are as homogeneous as possible. It will be assumed that only one primary unit is sampled from each stratum, and that the probability of selecting the j-th primary unit within the h-th stratum is proportionate to P_{hj}, where P_{hj} is the measure of size of the primary unit and is equal to the sum of the measures of size of the sub-areas that it contains. It will be assumed, also, that t_h, the over-all sampling ratio to be used within the h-th stratum, has been determined for all strata on the basis of considerations of optimum allocation.

The introduction of area substratification within primary strata may then be accomplished as follows:

(a) The sub-areas within each primary stratum are classified into substrata on the basis of their characteristics. (For example, they may be classified into predominantly farm and predominantly nonfarm sub-areas, and these further classified on the basis of the average size of farm or average rental value of the dwelling units. In such a case, the sub-areas within the primary stratum that are predominantly farm and that have average rental values lying within a specified interval constitute a substratum.)

(b) The sub-areas within the primary unit selected from each primary stratum are classified into the same substrata.

(c) Subsampling units are defined within each of the substrata within the selected primary units. The number of subsampling units defined within that part of the i-th substratum that is contained within the j-th primary unit is denoted by M_{hij}. (Various types of subsampling units may be defined, such as the individual person, farm, dwelling unit, or structure, a very small area, etc. The subsampling units need be defined only within the selected primary sampling units.)

(d) The number of subsampling units to be included in the sample from the i-th substratum within the selected (j-th) primary sampling unit is

$$m_{hij} = M_{hij} t_h P_{hi} / P_{hij}, \tag{5}$$

where P_{hij} is the measure of size of that part of the i-th substratum that lies within the j-th primary unit, and $P_{hi} = \sum_j P_{hij}$ is the sum of the measures of size of the sub-areas contained in the i-th substratum of the h-th primary stratum. This method of allocating the subsampling provides that the subsample drawn from the selected primary unit is representative, so far as possible, of the entire stratum, rather than of the particular primary unit that happens to be included in the sample from that stratum. To illustrate, suppose the numbers of persons in sub-areas from the 1940 census are used as the measures of their sizes, and that the sub-areas are classified into substrata on the basis of their characteristics in 1940 as indicated by the 1940 Decennial Census of Population. The allocation of the subsampling indicated above then provides that if the proportion of the total population residing in sub-areas that are predominantly farm is 30 percent, the sample will be drawn in such a manner that 30 percent of the 1940 population expected in the sample would be from the predominantly farm sub-areas, even though, in the selected primary sampling unit, perhaps only 15 percent of the 1940 population might reside in such areas.

(e) The population character to be estimated is

$$X = \sum_h^L \sum_i^{S_h} \sum_j^{Q_h} \sum_k^{M_{hij}} X_{hijk}, \tag{6}$$

where X_{hijk} is the aggregate value of a specified characteristic for all of the elements contained within the k-th subsampling unit in the i-th substratum of the j-th primary unit; S_h is the number of substrata and Q_h is the number of primary units in the h-th primary stratum; and L is the number of primary strata. (X might be the total number of workers in the United States, or the total number of farm laborers, etc.) An estimate of X from the sample is

$$X' = \sum_{h}^{L} 1/t_h \sum_{i}^{S_h} \sum_{k}^{m_{hij}} X_{hijk}. \tag{7}$$

No summation over j is involved, because only one primary unit is drawn from the h-th stratum. This is a very simple estimate, involving a sum weighted only at the primary strata level. If the t_h are all set equal to t, i.e., if a constant proportion is sampled from each stratum, the estimate becomes merely the total number of elements in the sample having the specified characteristic multiplied by $1/t$, the reciprocal of the sampling ratio.

The allocation of the subsampling indicated above may be deviated from and the controls of area substratification can still be maintained if proper modifications are made in the sample estimate. In this event, differential weighting must be introduced at the substrata level rather than only for the primary strata.

The definition of heterogeneous primary sampling units, the proper classification of them into strata, and the use of probabilities proportionate to the measures of size in the selection of the primary units are particularly desirable if area substratification is used. If these are not introduced the likelihood of making substantial gains through the use of area substratification is decreased. The definition of the primary strata should be made in conjunction with the definition of the substrata, and should insure that each primary unit has adequate representation of each substratum that is to be defined within that primary stratum. With this restriction observed, the number of significant substrata that can be defined will be limited by the heterogeneity of the primary units. Thus, in order to provide for substratification into predominantly farm and predominantly nonfarm areas, the primary sampling units should be defined so that both farm and nonfarm areas are represented in each unit. This procedure not only makes area substratification more effective, but improves the efficiency of the sample in making separate estimates for such classes of the population. However, if this procedure cannot be adhered to exactly in practice, primary units in which certain of the substrata are not represented will occasionally come into the sample. One alternative when this occurs is to combine certain substrata; another is to exclude such primary units from the sample.

Since the number of primary strata is restricted by the number of primary units to be sampled, it is wasteful to set up strata at the primary level with respect to sources of variation that can be controlled adequately through area

substratification. For example, if farm areas and nonfarm areas are to be distinguished in the substrata, the primary strata should not be exhausted by classifying the primary units into a large number of strata by percent farm (percent of total population in primary unit living on farms), since the effect of the substratification is to control the variation in the percentage farm. Limiting the number of percentage farm classes at the primary level makes possible the use of other modes of stratification that will control on farm type, or on the industrial character of the nonfarm population, or on some other similar criteria.

Area substratification is to be distinguished from the fairly commonly used method of specifying the number of elements to come into the sample from each of several different classes of elements—whether such quotas are fixed to make the sample correspond with the specified characteristics of the entire primary stratum or of the selected primary sampling unit. The method of fixing quotas and instructing interviewers or enumerators to obtain a given number of elements (persons, dwelling units, farms, voters, etc.) having various specified characteristics has a fundamental weakness that is avoided in area substratification within primary strata. Such quotas ordinarily must be set on the basis of previous information or rough estimates, and thus cannot accurately reveal changing characteristics of the population. Area substratification, on the other hand, uses previous information to insure the proper representation of various types of areas in the sample. The numbers of elements obtained with various specified characteristics are determined from the population as it is, and not as it was at some previous date. In times of rapid change the fixing of quotas on the basis of previous information may introduce increasingly serious biases.

The gain from using previously available information in stratifying areas arises from the fact that there is a high correlation in the characteristic of an area from time to time over a period of several years. An area that is predominantly farm at one date ordinarily will be predominantly farm a few years later. Similarly, while very substantial shifts in population may occur, the numbers of persons in a set of areas at one time ordinarily will be very highly correlated with the numbers a few years later. However, area substratification does not depend on the fact that no shifts occur. If shifts have occurred it will measure them. If the shifts have been sufficient to completely alter the character of most small areas, it will still provide estimates revealing the changing character of the population, but under these circumstances the efficiency of the method is decreased.

V—EXPECTED VALUES AND VARIANCES FOR THE SUBSAMPLING SYSTEM INCORPORATING THE PRINCIPLES OUTLINED ABOVE

The system of sampling incorporating the principles of enlarged primary units, the selection of primary units with probabilities proportionate to the measures of size and area substratification will be examined more fully below. It will be referred to, for convenience, as the specified subsampling system.

1. The expected value of an estimated total for the specified subsampling system. All summations in the formulas below are over the population unless otherwise indicated. The expected value of X' as defined in Eq. (7) is

$$EX' = \sum_h \sum_j \sum_i \sum_k (1/t_h)(P_{hj}/P_h)(m_{hij}/M_{hij})X_{hijk}.$$

From (5) $t_h = m_{hij}P_{hij}/M_{hij}P_{hi}$, and therefore

$$EX' = \sum_h \sum_j \sum_i \sum_k (P_{hi}/P_{hij})(P_{hj}/P_h)X_{hijk}$$

$$= \sum_h P_h \sum_j \sum_i (P_{hi}/P_h)(P_{hj}/P_h)(X_{hij}/P_{hij}) = \sum P_h R_{h(A)}$$

where

$$P_h = \sum_i P_{hi} = \sum_j P_{hj}; \qquad R_{h(A)} = \sum_j (P_{hj}/P_h)R_{hj(A)};$$

$$R_{hj(A)} = \sum_i (P_{hi}/P_h)R_{hij}; \quad \text{and} \quad R_{hij} = \sum_k X_{hijk}/P_{hij} = X_{hij}/P_{hij}.$$

The $R_{hj(A)}$ will be referred to as the adjusted ratio for the j-th primary unit. It is the weighted average within the j-th unit of the substrata ratios, R_{hij}, where the same set of weights P_{hi} is applied to the R_{hij} in each primary unit within a stratum. The $R_{h(A)}$ is the average, within the h-th stratum of the adjusted ratios. Hence

$$EX' = X + \sum_h P_h(R_{h(A)} - R_h), \tag{8}$$

where

$$R_h = X_h/P_h, \quad \text{with} \quad X_h = \sum_i \sum_j X_{hij},$$

is the ratio of the aggregate value of the specified characteristic for the elements in the h-th stratum to the measure of size of that stratum, and where the population character being estimated (6), is equal to $X = \Sigma X_h = \Sigma P_h R_h$.

From (8), it is seen that X' is a biased estimate of X, although ordinarily, in practice, only slightly so. The bias, equal to $\Sigma P_h(R_{h(A)} - R_h)$, is the sum of the biases for the various primary strata. Under many practical circumstances some of these will be slightly negative and some slightly positive, with the result that the total bias will be relatively small. The bias would be nonexistent if area substratification were not used, or if the form of the sample estimate were properly modified, but here again, as in the case of substituting biased for unbiased estimates discussed in Sec. III, the introduction of a slight bias may result in a substantial reduction in the variance.

A sufficient, although not necessary, condition for the sample estimate (7) with area substratification to be unbiased is for the ratios P_{hij}/P_{hj} to be uncorrelated with the R_{hij} within each substratum. Under these circumstances

$$\sum_j \frac{P_{hj}}{P_h}\frac{P_{hij}}{P_{hj}}R_{hij} = \sum_j \frac{P_{hj}}{P_h}\frac{P_{hij}}{P_{hj}} \sum_j \frac{P_{hj}}{P_h}R_{hij} = \frac{P_{hi}}{P_h}\sum_j \frac{P_{hj}}{P_h}R_{hj}$$

and therefore

$$R_h = \sum_i \sum_j \frac{P_{hj}}{P_h} \frac{P_{hij}}{P_{hj}} R_{hij} = \sum_i \sum_j \frac{P_{hi}}{P_h} \frac{P_{hj}}{P_h} R_{hij} = R_{h(A)} .$$

To illustrate, if the measures of size are the 1940 populations, then the sample estimate will be unbiased if the proportions of the 1940 populations of the primary sampling units that are in the various substrata are uncorrelated with the corresponding R_{hij}. As indicated earlier these conditions are approximated in many practical problems, especially if the primary stratification has been carried out effectively. Moreover, if the conditions are not met approximately, the bias introduced may still be very small. (See Sec. VII for a numerical illustration.)

2. The mean square error of an estimated total for the specified subsampling system. For the development of the mean square error of X' for the specified subsampling system, see the Appendix, Section 2. There it is shown that the mean square error of X' is

$$\sigma^2_{X'} = \sum_h \sum_i \sum_j P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \frac{\sigma^2_{hij}}{m_{hij} \overline{P}^2_{hij}}$$

(9)

$$+ \sum_h P_h^2 \sum_j \frac{P_{hj}}{P_h} (R_{hj(A)} - R_{h(A)})^2 + [\sum P_h (R_{h(A)} - R_h)]^2$$

where

$$\sigma^2_{hij} = \sum_k (X_{hijk} - \bar{X}_{hij})^2 / M_{hij}$$

is the variance between subsampling units within a substratum of the aggregate value of a specified characteristic for the subsampling unit and

$$\overline{P}_{hij} = P_{hij} / M_{hij}$$

is the average measure of size of the subsampling units in the h-i-j-th area.

The first term of (9) is the contribution of the variance between subsampling units and may be kept small by proper definition of the subsampling units, and, of course, by increasing the subsampling ratio. The second term of (9) is the contribution of the variance between primary sampling units within strata; and the third term is the contribution of the bias, which, as indicated before, ordinarily will be of negligible size, so that the mean square error and the variance will be approximately equal.

It is the variance between primary sampling units that contributes most heavily to the total variance in many subsampling situations, and it is on this contribution that the modifications proposed in this paper have their principal effect. The effect of area substratification is seen by comparing the variance between primary units given above with that obtained if area substratification were not used but other aspects of the design remained unchanged. In this

event the variance between primary units involves the variance of the ratio, $R_{hj} = \sum_i X_{hij}/P_{hj} = X_{hj}/P_{hj}$, instead of the variance of the adjusted ratio, $R_{hj(A)}$.

The relationship between the variance of R_{hj} and that of $R_{hj(A)}$ within the h-th primary stratum is given by

$$\sigma^2_{R_{hj}} = \sigma^2_{R_{hj(A)}} + \sigma^2_{R_{hj}-R_{hj(A)}} + 2\rho\sigma_{R_{hj(A)}}\sigma_{R_{hj}-R_{hj(A)}}, \tag{10}$$

where $\sigma^2_{R_{hj}-R_{hj(A)}}$ is the variance of the difference between the adjusted and the unadjusted ratios, and ρ is the correlation between the adjusted ratio and the amount of the adjustment. Thus, if the correlation is near zero or positive, there will be a gain from the introduction of area substratification, although there may be a loss if the correlation is highly negative. Essentially, the condition for ρ being equal to or near zero is the same as that for the sample estimate being unbiased; namely, that the P_{hij}/P_{hj} be uncorrelated or only slightly correlated with the R_{hij} within each substratum.[3]

The variance of $R_{hj(A)}$ rather than that of R_{hj} occurs in the variance of X' because the subsampling numbers were allocated proportionate to the P_{hi}, no matter what primary sampling unit happened to be selected for inclusion in the sample. The ratio R_{hj} like $R_{hj(A)}$ may be regarded as the weighted average of the R_{hij} but with the weights equal to P_{hij} instead of P_{hi}, and thus varying from primary unit to primary unit. It would appear, therefore, from the relationship of the variances given above, that if the substrata are effective, and if the P_{hij} are highly correlated with the actual sizes of the substrata, the weighted average using fixed weights in all primary units should have a considerably smaller variance than that using variable weights. This turns out to be the case in many practical situations, some illustrations of which will be given later (see Sec. VII).

3. The mean square error of ratio estimates for the specified subsampling system. The need for estimating a ratio from a sample arises in two cases; first, when the ratio is the population character for which an estimate is desired, and second, when the application of a ratio from the sample to a known total uses additional available information for obtaining an improved estimate of the desired total.

Ratio estimates are desired as an end-result when, for example, the change in a characteristic from one time to another is being considered. Thus, if Y' is the estimated total income of farm workers at one date, and X' the corresponding estimated total income at a second date, then $r' = X'/Y'$ is an estimate of the relative change in the total income of farm workers over the period of time covered. Similarly, the estimate of a percentage such as the percentage of the

[3] Actually, a sufficient, although not necessary, condition for ρ to be equal to zero is that P_{hij}/P_{hj} be uncorrelated with both the ratio R_{hij} and the cross-product $R_{hij}R_{hgj}$ for all pairs of substrata.

workers unemployed will involve the ratio of two random variables from the sample. Ratio estimates from a sample may be particularly useful in instances where the reliability of the ratio estimate is greater than the reliability of the estimate of either the numerator or the denominator, as is frequently the case.

Ratio estimates may be used as a means of obtaining an estimated aggregate value of a specified characteristic, if Y, the aggregate value of a second characteristic highly correlated with X is known exactly from independent sources, and X' and Y', estimates of X and Y respectively, are available from the sample. Thus

$$X'' = [X'/Y']Y = r'Y \tag{11}$$

is an estimate of the aggregate value of the specified characteristic. If the correlation, in successive samples, between X' and Y' is sufficiently high, the ratio estimate will be a more efficient estimate of X than will X', the simple estimated total given earlier (7); but X' will prove the more reliable estimate when the correlation is low.[4] Thus, X'', when the correlation between X' and Y' is sufficiently high, makes use of more of the relevant available information for estimating X than does X'.

The application of ratio estimates to the specified subsampling system is considered below.

(*a*) *The estimated ratio and its mean square error.* The estimate of the population ratio $r = X/Y$ is:

$$r' = \frac{X'}{Y'} = \frac{\sum_h^L \frac{1}{l_h} \sum_i^{S_h} \sum_j^1 \sum_k^{m_{hij}} X_{hijk}}{\sum_h^L \frac{1}{l_h} \sum_i^{S_h} \sum_j^1 \sum_k^{m_{hij}} Y_{hijk}}, \tag{12}$$

where X' is given in (7) above, and Y' is a similar estimate of the total value of a second characteristic. The mean square error of r' is approximately

$$\begin{aligned} \sigma_{r'}^2 = \frac{1}{Y^2} \Bigg\{ & \sum_h \sum_i \sum_j P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \frac{\sum_k Y_{hijk}^2 (r_{hijk} - r_{hij})^2}{m_{hij} M_{hij} \overline{P}_{hij}^2} \\ & + \sum_h \sum_i \sum_j P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \sigma_{hij:Y}^2 \frac{(r_{hij} - r)^2}{m_{hij} \overline{P}_{hij}^2} \\ & + \sum_h P_h^2 \sum_j \frac{P_{hj}}{P_h} R_{hj(A):Y}^2 (\bar{r}_{hj(A)} - \bar{r}_{h(A)})^2 \\ & + \sum_h P_h^2 (\bar{r}_{h(A)} - r)^2 \sum_j \frac{P_{hj}}{P_h} (R_{hj(A):Y} - R_{h(A):Y})^2 \Bigg\} \end{aligned} \tag{13}$$

[4] The variance of the ratio of random variables of the form $r' = X'/Y'$ is approximately $\sigma_{r'}^2 = r^2(V_{X'}^2 + V_{Y'}^2 - 2\rho_{X'Y'}V_{X'}V_{Y'})$ where V indicates the coefficient of variation of the variable designated by the subscript, and $\rho_{X'Y'}$ is the correlation. Hence, if $\rho_{X'Y'}$ is sufficiently large $V_{r'}^2$ will be less than $V_{X'}^2$. The size of $\rho_{X'Y'}$ required depends on the relative magnitudes of the coefficients of variation of X' and Y'.

where

X_{hijk} = the aggregate value of a specified characteristic for the elements in the k-th subsampling unit within the h-i-j-th area, for which a total is to be estimated;

Y_{hijk} = the aggregate value of a second specified characteristic for the elements in the same subsampling unit, and for which the total in the population is known;

$$Y_{hij} = \sum_k Y_{hijk}, \quad \text{and} \quad Y_h = \sum_i \sum_j Y_{hij}.$$

$$\sigma^2_{hij:Y} = \frac{\sum_k (Y_{hijk} - \bar{Y}_{hij})^2}{M_{hij}}$$ is the variance of the sampling units in the h-i-j-th area with respect to the second characteristic, and $\bar{Y}_{hij} = Y_{hij}/M_{hij}$.

$$R_{hj(A):Y} = \sum \frac{P_{hi}}{P_h} \frac{Y_{hij}}{P_{hij}}$$ is the adjusted average of the Y_{hij}, and

$$r_{hijk} = \frac{X_{hijk}}{Y_{hijk}}, \quad r_{hij} = \frac{X_{hij}}{Y_{hij}},$$ etc., are the ratios of the X to the Y for the areas indicated by the subscripts, and

$$\bar{r}_{hj(A)} = \frac{R_{hj(A)}}{R_{hj(A):Y}}, \quad \text{and} \quad \bar{r}_{h(A)} = \frac{R_{h(A)}}{R_{h(A):Y}}$$ are the ratios of the adjusted ratios for X and Y indicated by the subscripts;

and the remaining symbols are as defined in the sections above where the expected value and variance of X' are given.

The first and third terms of (13) are, ordinarily, the principal contributing terms. The second and fourth terms contain contributions due to the variation between the means of the substrata and the primary strata respectively even though the sample was stratified with respect to these classes. In some instances, the contributions of these terms will be important. The between strata contributions arise because the primary and subsampling units vary in size with respect to the character Y.

This formula for the mean square error of a ratio is approximately equal to the one more commonly used given in footnote 4. The two formulas, both of which are approximations, would be identical if certain terms which are ordinarily negligible were retained in (13). This latter formula has the advantage of indicating the effect of different aspects of the design of the sample on the variance of the ratio. The derivation of this approximate variance formula is given in the Appendix, Section 3, together with an indication of the accuracy of the approximation.

(*b*) *The estimated totals and their mean square errors.* As mentioned earlier, two estimates of X, the aggregate value of a given characteristic for all elements are X' (7), and X'' (11). The mean square error of X' is given by (9) and that of X'' is simply equal to $Y^2\sigma^2_{r'}$, where $\sigma^2_{r'}$ is given approximately by (13).

The decision as to whether to use X' or X'' as an estimate of X depends, of course, in the first instance, on whether Y is known, and in the second instance, on the relative magnitudes of the respective mean square errors given in (9) and (13). These may be approximated from prior knowledge concerning the relationships in the population under investigation, or they may be estimated from preliminary sample investigations. However, in instances where there is a positive correlation between the X_{hijk} and the Y_{hijk} within substrata, it is fairly safe to assume that if the information necessary for the ratio estimate is available, there will be little to lose and possibly considerable to gain from its use.

The use of (11) instead of (7) is often desirable when Y in (11) is the aggregate value of the actual sizes of the primary units, and Y' is its estimate. This is particularly so if the measures of size used are not fairly precise measures of the actual sizes, and if, at the same time, the actual size is highly correlated with the character being estimated, in which case the use of ratio estimates will yield gains in both the between primary unit contribution and the within primary unit variance. (See Sec. VII for numerical illustrations.) However, if the measures of size are identical with the actual sizes (i.e., $P_{hijk} = Y_{hijk}$) the last two terms of (13) are identical with the between primary unit contribution to the variance of X' (9), and only the within primary unit variance is affected by the ratio estimate.

While it is fairly safe in practice, if Y is known, to make use of X'' instead of X' as the estimate of X, some care must be exercised to make sure that the X_{hijk} has at least a moderately high average correlation with the Y_{hijk}, where the correlations considered are those within substrata within primary sampling units. If this correlation is low, and if the size of the subsampling unit varies considerably, the ratio estimate may be considerably less efficient than the simple total estimate. On the other hand, if the measures of size of the various substrata and of the primary sampling units are fairly close measures of the actual size, and if the subsampling units have been carefully defined so that they do not vary too greatly in size, the two estimates are likely to have about the same efficiency.

VI—SOME PHYSICAL PROPERTIES OF FREQUENTLY OCCURRING POPULATIONS THAT ARE BASIC TO THE SAMPLING PRINCIPLES RECOMMENDED IN THIS PAPER

Many actual populations are characterized by the following physical properties:

(i) The elements within a cluster are positively correlated with regard to a specified characteristic.

(ii) Clusters containing large numbers of elements have greater internal heterogeneity than clusters containing small numbers of elements.

(iii) Increasing the size of the cluster brings in correlated elements (e.g., in population or agriculture surveys larger clusters are formed by including households or farms in adjacent areas).

The first of these properties is recognized implicitly in the literature where the losses of efficiency through the use of large clusters as sampling units are frequently cited. In our experience the second and third properties hold just as commonly in actual populations, and ordinarily for the same populations for which the first property holds.

The presence of these physical properties in combination within strata leads to the following mathematical relationships that have been used throughout this paper:

(a) The sizes of the primary sampling units, N_{hj}, are negatively correlated with the ρ_{hj}, the intra-class correlations between elements within the units;
(b) The N_{hj} and $N_{hj}\rho_{hj}$ are positively correlated;
(c) The N_{hj} and σ^2_{hj} are positively correlated;
(d) The N_{hj} and σ^2_{hj}/N_{hj} are negatively correlated.

The use of these relationships has determined most of the choices among alternative procedures throughout this paper. The relationships, of course, do not necessarily hold, and exceptions to them can be found [5]. The frequent occurrence of populations characterized by such properties justifies further research on the more effective use of these and other properties that may be found to hold.

VII—SOME APPLICATIONS OF THE PRINCIPLES DESCRIBED IN THIS PAPER TO AN ACTUAL SAMPLING PROBLEM

The analyses summarized below were carried out for the purpose of deciding between alternative sampling procedures in the revision of a monthly national sample for labor force and other characteristics. Budgetary and administrative restrictions made it necessary to confine the field operations to a limited number of administrative centers scattered over the country, from which a sample of less than one-tenth of one percent of the population of the United States was to be drawn.

The original sample (the one to be revised) was of a usual subsampling design in which counties were used as the primary sampling units, and households or small clusters of households were used as the subsampling units. In the revised sample contiguous counties were combined wherever administratively feasible, to form more heterogeneous primary units than the individual counties. Approximately 2000 primary sampling units were formed from the 3000 counties in the United States. The combinations of counties, the primary stratification, the area substratification, and the measures of size, were determined on the basis of 1940 Decennial Census data together with more recent data where available.[5]

The applications of the various principles suggested in this paper have been

[5] See [11] for a full description of the proposed revised sample, including an outline of the criteria of stratification used. That paper may be useful as a simple description of an application of the specified subsampling system.

evaluated by estimating 1930 Census labor force characteristics from a sample that was stratified on the basis of 1940 and more recent data. This constituted a particularly severe test of some of the methods, because of the substantial shifts that had taken place during the 10-year interval between 1930 and 1940.

The analyses to be summarized in this section are concerned primarily with the gains obtainable under favorable circumstances by the introduction of three sampling principles; namely,

(1) enlarged primary units (see Sec. IV-1);
(2) the sampling of primary units with probability proportionate to measures of their size (see Sec. IV-2);
(3) area substratification (see Sec. IV-3).

Some comparisons are also given to illustrate the effect of using alternative sample estimating formulas. Computations have been made for six of the principal items that are currently being included in a monthly report of the labor force; namely, total numbers of male and female workers, total numbers of male and female agricultural workers, and total numbers of male and female nonagricultural workers. The comparisons between alternative systems have been made holding constant both the primary stratification criteria and the expected numbers of persons to be drawn into the sample.

The percentage gains given below are the reductions in the *between* primary unit contributions (which include the bias contributions) to the mean square error.[6] Except where otherwise specified, the sample estimate used is given by (7).

1. Gains obtained by introducing enlarged primary units. The gains obtained by using enlarged primary units are calculated by comparing the mean square errors arising from the sampling design in which individual counties are primary units with the mean square errors arising from the design in which combinations of counties are the primary units. In both designs, the primary units are drawn with equal probabilities and no area substratification is used. For this comparison, preliminary computations have been completed for only a limited number of strata and for two of the labor force items given above; namely, total male workers and total female workers. The reduction in the sampling errors obtained by introducing enlarged primary units is estimated to be 48 per cent for total male workers and 26 per cent for total female workers.

2. Further gains obtained by introducing probability proportionate to measures of size. The further gains obtained by using the principle of sampling with probability proportionate to measures of size are calculated by comparing the mean square errors arising from the design in which the units are drawn with

[6] The contribution of the variance *within* the primary units to the total mean square error was relatively small in all instances, and practically unaffected by the introduction of the various principles.

equal probability with the mean square errors arising from the design in which the units are drawn with probability proportionate to measures of size. In both the designs, the primary units are combinations of counties, and in neither of them is area substratification used. The estimated per cent gains are as follows:

Total Workers		*Agricultural Workers*		*Nonagricultural Workers*	
Male	*Female*	*Male*	*Female*	*Male*	*Female*
50	8	77	6	19	21

The gains reflect both decreases in the sampling variance and the elimination of the bias which arises when the primary units are drawn with equal probabilities.[7]

3. Further gains obtained by introducing area substratification. The further gains obtained by using the principle of area substratification are calculated by comparing the mean square errors for the design in which area substratification is not used, with those for the design in which area substratification is introduced. In both these designs the primary units are combinations of counties, and are drawn with probability of selection proportionate to measures of their sizes. The estimated per cent gains are as follows:

Total Workers		*Agricultural Workers*		*Nonagricultural Workers*	
Male	*Female*	*Male*	*Female*	*Male*	*Female*
6	31	46	51	32	22

4. Gains obtained by the integration of the above principles into a single subsampling system (the specified subsampling system). The gains obtained by using all three principles are calculated by comparing the mean square errors for the specified subsampling system (in which all three principles are used) with the mean square errors for the system in which none of these principles is used. In the specified subsampling system, combined counties are the primary units, the primary units are drawn with probability proportionate to measures of their size, and area substratification is used. In the other system, the primary units are individual counties, the sampling is done with equal probabilities and area substratification is not used. Preliminary computations for this comparison are available for only 2 of the 6 labor force items; namely, total male and total female workers. The estimated gains were 76 per cent for male workers and 53 per cent for female workers.

[7] As indicated before, estimate (7) is used in both designs compared above. This estimate is unbiased for the design in which the primary units are drawn with probability proportionate to measures of size, but is biased for the design in which they are drawn with equal probabilities. However, for the latter design, the biased estimate is usually much more efficient than the best linear unbiased estimate. For the six labor force items, the best linear unbiased estimate gives rise to variances that are several times as large as the mean square errors for the biased estimate.

Calculations are available for all 6 items to measure the gains obtained by the use of the last two of the principles in combination; namely, probability proportionate to measures of size and area substratification. For measuring these gains, the systems are as described above, except that in both designs the primary units are combinations of counties. The estimated per cent gains are as follows:

Total Workers		*Agricultural Workers*		*Nonagricultural Workers*	
Male	*Female*	*Male*	*Female*	*Male*	*Female*
54	37	88	54	45	39

While both the specified subsampling system and the alternative to which it was just compared are biased designs, the bias in the specified system is appreciably smaller than the bias in the latter. For example, while the bias of the specified system in the estimation of total male workers was less than one-half per cent of the true total male workers, the bias for the alternative design in the estimation of the same population character was more than one and one-half per cent.

5. The choice of estimate to use with the specified subsampling system. The simple estimate (7) given for the specified subsampling system may be improved on by the use of regression techniques (see Sec. III). However, such techniques may require a great deal of clerical work, so that they frequently cannot be used in practice. As indicated in the last part of Sec. V, however, if certain independent information such as a knowledge of the total population is available, a simple ratio estimate of the form of (12) may sometimes introduce gains over (7). The use of the ratio estimate may be particularly desirable when the correlation between the measures of size and the actual sizes of the primary sampling units is only moderately high, and when, at the same time, the actual sizes are highly correlated with the values for the character being estimated. A small-scale experiment in the sampling for labor force items indicated that for estimating total male workers for 1930, both the variance between primary units and the variance within primary units for the ratio estimate (12) were approximately one-half that for the simple estimate (7). The use of the ratio estimate had very little effect in the estimation of the remaining five labor force characteristics. The reduction in variance of the total male employment figure was brought about because migration since 1930 reduced the correlation between the 1930 and 1940 sizes, and furthermore, the number of male workers is highly correlated with the total population. Similar reductions for the variances of the other five items were not obtained because the correlations with actual sizes for the other items were not as high.

6. Some final remarks. The gains just obtained arose from application of the sampling principles enumerated above. The situations that these principles were applied to are favorable, but are frequently met in practice. The principles differ in their effect depending on the particular attributes of the population

being studied. The use of enlarged primary units may be desirable whenever the enlarged units are internally more heterogeneous than are the smaller units. The selection of primary units with probability proportionate to size is desirable for the general classes of populations described in Sec. VI whenever the primary units vary considerably in size. The use of area substratification is limited to sampling situations where large primary units are used. The joint effect of all three principles shows to greatest advantage when subsampling is used, the primary units are large, but variable in size, and the number of primary units included in the sample is limited by cost or administrative conditions. The types of estimates described in Sec. III may be effective in a large number of physical situations other than those mentioned in this paper.

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APPENDIX

1. The effect of the consolidation of the primary units on the sampling variance (see Sec. IV-1). Let $\bar{X}_1' = \sum_{j}^{q} \sum_{k}^{n} X_{jk}/qn$, be the average for the sample where the primary units are the original units and where X_{jk} is the value of the k-th element in the j-th primary unit; q is the number of primary units in the sample, and n is the number of elements sampled from each of the q primary units. The variance of $\bar{X}_1'$ is

$$\sigma^2_{\bar{x}_1} = \frac{N-n}{(N-1)nq}\sigma^2_{1w} + \frac{Q-q}{(Q-1)q}\sigma^2_{1b} \tag{14}$$

where Q is the number of original primary units in the population; N is the number of elements in each original primary unit; $\sigma^2_{1w} = \Sigma\Sigma(X_{jk} - \bar{X}_j)^2/QN$ is the variance within the original primary units, with $\bar{X}_j = \sum_{k} X_{jk}/N$; and $\sigma^2_{1b} = \Sigma(\bar{X}_j - \bar{X})^2/Q$ is the variance between the original primary units, with $\bar{X} = \Sigma\bar{X}_j/Q$.

$\sigma^2 = \Sigma\Sigma(X_{jk} - \bar{X})^2/QN = \sigma^2_{1w} + \sigma^2_{1b}$. Then (15)

$$\sigma^2_{1b} = \sigma^2[1 + \rho_1(N-1)/N \tag{16}$$

where $\rho_1 = \left[\sigma_{1b}^2 - \frac{\sigma_{1w}^2}{N-1}\right]\frac{1}{\sigma^2}$ is the intra-class correlation[8] between elements in the original units.
From (15) and (16)

$$\sigma_{1w}^2 = \frac{N-1}{N}\sigma^2(1-\rho_1). \tag{17}$$

Hence

$$\sigma^2_{\bar{X}'} = \frac{N-n}{N}\frac{\sigma^2}{nq}(1-\rho_1) + \frac{Q-q}{(Q-1)q}\frac{\sigma^2}{N}[1+\rho_1(N-1)]. \tag{18}$$

Similarly, the variance of $\bar{X}_2'$ is

$$\sigma^2_{\bar{X}_2'} = \frac{CN-n}{CN}\frac{\sigma^2}{nq}(1-\rho_2) + \frac{Q-qC}{(Q-C)q}\frac{\sigma^2}{CN}[1+\rho_2(CN-1)] \tag{19}$$

where $\bar{X}_2'$ is the mean for the enlarged primary units, ρ_2 is the intra-class correlation between elements in the enlarged primary units and C is the number of original units combined to form each enlarged unit. Then

$$\sigma^2_{\bar{X}_1'} - \sigma^2_{\bar{X}_2} = \frac{\sigma^2}{qN}\left\{\frac{(q-1)(C-1)}{(Q-1)(Q-C)} + \rho_1 a_1 - \rho_2 a_2\right\} \tag{20}$$

where $a_1 = \frac{(Q-q)(N-1)}{Q-1} - \frac{N-n}{n}$ and $a_2 = \frac{(Q-Cq)(CN-1)}{(Q-C)C} - \frac{CN-n}{Cn}$.

Since

$$a_1 - a_2 = \frac{(C-1)(q-1)(QN-1)}{(Q-1)(Q-C)} \geqq 0 \quad \text{and} \quad \frac{(q-1)(C-1)}{(Q-1)(Q-C)} \geqq 0,$$

then a gain is brought about by enlarging primary units whenever $\rho_1 > \rho_2$, where ρ_1 and ρ_2 are both positive.

2. Comparison of variances of certain alternative subsampling systems where the primary units are of unequal sizes. The development of (4), the formula for the difference between the variances of sample estimates compared in Sec. IV-2 is given below. We shall confine ourselves to the simple case where only one primary sampling unit is drawn into the sample from each stratum. Let

$$\bar{X}' = \Sigma N_h \bar{X}_h'/N \tag{21}$$

be the sample estimate used for each of the three designs to be compared, where $\bar{X}_h' = \bar{X}_{hj}' = \sum_k^{n_{hj}} X_{hjk}/n_{hj}$, and X_{hjk} is the value of the k-th element in the j-th

[8] For definitions and properties of intra-class correlations, see Secs. 38–40 of *Statistical Methods for Research Workers*, R. A. Fisher, and [5].

primary unit in the h-th stratum; L is the number of strata; n_{hj} is the number of elements drawn into the sample from the j-th primary unit in the h-th stratum with N_{hj} the corresponding total number, $N_h = \sum_j^{Q_h} N_{hj}$ with Q_h = the number of primary units in the h-th stratum, and $N = \sum_h^L N_h$. If the subsampling within a stratum is of a constant proportion, C, as in the first of the subsampling systems mentioned, n_{hj} in the above estimate is equal to $C\,N_{hj}$. If the subsampling within a stratum is of a constant number, as in the second subsampling system mentioned, as well as in the recommended system, n_{hj} is equal to $\bar{n}_h = C\sum_j N_{hj}/Q_h = C\bar{N}_h$.

We shall denote the sample estimate for the first design by $\bar{X}_1'$, that for the second design by $\bar{X}_2'$, and that for the recommended design by $\bar{X}_3'$.

The expected values of the sample estimates for the first two designs, $\bar{X}_1'$, and $\bar{X}_2'$, are the same, and are equal to

$$E\bar{X}_1' = E\bar{X}_2' = \bar{X} = \frac{1}{N}\sum_h \frac{N_h}{Q_h}\sum_j \frac{n_{hj}}{N_{hj}}\sum_k \frac{X_{hkj}}{n_{hj}} = \frac{1}{N}\sum_h \frac{N_h}{Q_h}\sum_j \bar{X}_{hj}$$

where $\bar{X}_{hj} = \sum_k X_{hjk}/N_{hj}$. Thus, since $\bar{X}$ is not, in general, equal to $\sum_{h,i,j} X_{hij}/\sum_{h,j} N_{hj} = \bar{X}$, both $\bar{X}_1'$ and $\bar{X}_2'$ are biased estimates of $\bar{X}$.

For the recommended design, in which the primary unit is drawn with probability of selection proportionate to size and a constant number taken from the sampled units within a stratum, the expected value of the sample estimate is

$$E\bar{X}_3' = \frac{1}{N}\sum_h \sum_j N_h \frac{N_{hj}}{N_h}\frac{\bar{n}_h}{N_{hj}}\frac{X_{hj}}{\bar{n}_h} = \frac{1}{N}\sum_h\sum_j X_{hj} = \bar{X} \tag{22}$$

and therefore the estimate for the recommended design is unbiased.

The mean square error of $\bar{X}_1'$ is

$$\sigma^2_{\bar{X}_1'} = \frac{1}{N^2}\sum_h \frac{N_h^2}{Q_h}\left[\sum_j \frac{N_{hj}-n_{hj}}{(N_{hj}-1)n_{hj}}\sigma_{hj}^2 + \sum_j (\bar{X}_{hj}-\bar{X}_h)^2\right] + (\bar{X}-\bar{X})^2 - \frac{1}{N^2}\sum_h N_h^2(\bar{X}_h-\bar{X}_h)^2 \tag{23}$$

where $\sigma_{hj}^2 = \sum_k (X_{hjk}-\bar{X}_{hj})^2/N_{hj}$ is the variance between elements within the j-th primary sampling unit of the h-th stratum, $\bar{X}_h = \sum_j \bar{X}_{hj}/Q_h$, $\bar{X}_{hj} = X_{hj}/N_{hj}$, and $\bar{X}_h = \sum_j\sum_k X_{hjk}/\sum_j N_{hj} = \sum_j N_{hj}\bar{X}_{hj}/\sum_j N_{hj}$. The first term in the square bracket of (23) is the contribution of the variance within primary units. The second term in the square bracket is an approximation to the mean square error between primary units and the remaining terms give the error in this approximation. The mean square error of $\bar{X}_2'$ is given by the same formula but with n_{hj} replaced by $\bar{n}_h$.

The difference between $\sigma^2_{\bar{x}_1'}$ and $\sigma^2_{\bar{x}_2'}$ is

$$(24) \qquad \sigma^2_{\bar{x}_1'} - \sigma^2_{\bar{x}_2'} = \frac{1}{CN^2} \sum_h \frac{N_h^2}{Q_h} \sum_j \sigma_{hj}^2 \frac{N_{hj}}{N_{hj} - 1} \left(\frac{1}{N_{hj}} - \frac{1}{\bar{N}_h} \right),$$

which will be positive if σ_{hj}^2/N_{hj} is negatively correlated with N_{hj}, as is almost invariably the case in practice (see Sec. VI). Thus, since $\sigma^2_{\bar{x}_1'}$ ordinarily is larger than $\sigma^2_{\bar{x}_2'}$, it will suffice to compare $\sigma^2_{\bar{x}_2'}$ with $\sigma^2_{\bar{x}_3'}$ to show that the recommended subsampling system is more efficient than either of the first two mentioned.

The variance for the recommended design is

$$(25) \qquad \sigma^2_{\bar{x}_3'} = \frac{1}{N^2} \sum_h N_h^2 \left[\sum_j \frac{N_{hj}}{N_h} \frac{N_{hj} - \bar{n}_h}{N_{hj} - 1} \frac{\sigma_{hj}^2}{\bar{n}_h} + \sum_j \frac{N_{hj}}{N_h} (\bar{X}_{hj} - \bar{X}_h)^2 \right].$$

For comparing the mean square error of $\bar{X}_2'$ with the variance of $\bar{X}_3'$ we shall define

$$\rho_{hj} = \frac{1}{\sigma_h^2} \left[(\bar{X}_{hj} - \bar{X}_h)^2 - \frac{\sigma_{hj}^2}{N_{hj} - 1} \right]$$

as the intra-class correlation coefficient between elements within the j-th primary unit, where σ_h^2 is the variance between all elements within the h-th stratum. In this comparison, the terms outside the square brackets in (23), have been ignored because their contribution to the mean square error is either positive or negligible. Then,

$$(26) \qquad \sigma^2_{\bar{x}_2'} - \sigma^2_{\bar{x}_3'} = \frac{1}{N^2} \sum_h \frac{N_h^2}{Q_h} \left\{ \sum_j \frac{N_{hj}}{N_{hj} - 1} \frac{\sigma_{hj}^2}{\bar{n}_h} \left(1 - \frac{N_{hj}}{\bar{N}_h} \right) + \sigma_h^2 \sum_j \rho_{hj} \left(1 - \frac{N_{hj}}{\bar{N}_h} \right) \right\}.$$

The second term of this difference was given in Sec. IV-2 as the approximate difference, and the first term was neglected. To examine the relative magnitudes of the two terms we shall write

$$(27) \qquad \frac{N_{hj}}{N_{hj} - 1} \sigma_{hj}^2 = \sigma_h^2 (1 - \delta_{hj}).$$

Then

$$(28) \qquad \sigma^2_{\bar{x}_2'} - \sigma^2_{\bar{x}_3'} = \frac{1}{N^2} \sum_h \frac{N_h^2}{Q_h} \sigma_h^2 \left\{ \frac{1}{\bar{n}_h} \sum_j \delta_{hj} \left(\frac{N_{hj}}{\bar{N}_h} - 1 \right) - \sum_j \rho_{hj} \left(\frac{N_{hj}}{\bar{N}_h} - 1 \right) \right\}.$$

For the general class of populations given in Sec. VI the covariance between δ_{hj} and N_{hj}, and also that between ρ_{hj} and N_{hj}, will be negative. Moreover, in many practical problems of this class the two covariances will be of approximately the same magnitude. In such instances the first term of (27) will be equal to $\frac{1}{\bar{n}_h}$ times the second, and thus smaller than the second term for all $\bar{n}_h > 1$, and much smaller for moderately large values of $\bar{n}_h$. For example, in popula-

tions made up of clusters of different sizes for which the conditional probability of an element having a particular property for a fixed size of cluster is the same for all sizes of clusters, the two covariances will be very nearly equal. A number of practical problems approximate this situation. Moreover, even in the situations where the covariance of δ_{hj} and N_{hj} is several times that of ρ_{hj} and N_{hj}, say 5 times as large, then the second term will be larger than the first for all $\bar{n}_h > 5$.

Some numerical illustrations of the gains obtained through the use of the recommended system are given in Sec. VII, and for some of the items for which results are summarized in that section the gains were substantial.

3. The derivation of the variance formulas (13) and (9). The mean square error of a ratio of random variables is generally approximated from Taylor's expansion. If X' and Y' are random variables, $Y' > 0$, and r is the population character of which $X'/Y' = r'$ is an estimate, then

$$E\left\{\frac{X'}{Y'} - r\right\}^2 = E\,\frac{Y'^2}{(EY')^2}\left(\frac{X'}{Y'} - r\right)^2 + E\left(1 - \frac{Y'^2}{(EY')^2}\right)\left(\frac{X'}{Y'} - r\right)^2. \tag{29}$$

The first term in the right-hand side of (29) is a first approximation to the mean square error from Taylor's expansion, and the second term is the error in this approximation.

Eq. (13), and as a special case (9), is derived as follows:

$$E(r' - r)^2 = E\left\{\frac{\sum_h^L \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} X_{hijk}}{\sum_h^L \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} Y_{hijk}} - r\right\}^2. \tag{30}$$

Let $\psi_{hijk} = Y_{hijk}(r_{hijk} - r)$, and $Y' = \sum_h^L \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} Y_{hijk}$. Then, setting

$$\theta = \sum_h^L \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} \psi_{hijk}\Big/E\left(\sum_h^L \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} Y_{hijk}\right) = \frac{Y'}{EY'}\left(\frac{X'}{Y'} - r\right) \tag{31}$$

$$E\theta^2 = EY'^2(r' - r)^2/(EY')^2$$

is the first approximation to the mean square error.

Since EY' is evaluated in the same way as EX'(8), it is merely necessary to evaluate $EY'^2(r' - r)^2$, the numerator of $E\theta^2$. Now

$$EY'^2(r' - r)^2 = E\left[\sum_h \frac{1}{l_h}\sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} \psi_{hijk}\right]^2$$

$$= E\sum_h \frac{1}{l_h^2}\psi_h'^2 + E\sum_{\substack{h,q \\ h\neq q}} \frac{\psi_h'}{l_h}\frac{\psi_q'}{l_q}$$

where $\psi_h' = \sum_i^{S_h}\sum_j^{1}\sum_k^{m_{hij}} \psi_{hijk} = \sum_i^{S_h} \psi_{hi}'$.

Since $E\sum \frac{1}{t_h^2}\psi_h'^2 = E\sum_h\sum_i \psi'^2_{hi}/t_h^2 + E\sum_h \sum_{\substack{i,r\\ i\neq r}} \psi'_{hi}\psi'_{hr}/t_h^2$

$$EY'^2(r'-r)^2 = E\sum_h \frac{1}{t_h^2}\sum_i \psi_{hi}'^2 + E\sum_h \frac{1}{t_h^2}\sum_{\substack{i,r\\ i\neq r}} \psi'_{hi}\psi'_{hr} + E\sum_{\substack{h,q\\ h\neq q}} \frac{\psi'_h}{t_h}\frac{\psi'_q}{t_q}. \tag{32}$$

The first term in the right-hand side of (32) is

$$\begin{aligned} E\sum_{h,i}\psi'^2_{hi}\frac{1}{t_h^2} &= \sum_{h,i,j}\frac{1}{t_h^2}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\frac{M_{hij}-m_{hij}}{M_{hij}-1}\sum_k \psi^2_{hijk} \\ &\quad + \sum_{h,i,j}\frac{1}{t_h^2}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\frac{m_{hij}-1}{M_{hij}-1}\Big(\sum_k \psi_{hijk}\Big)^2. \end{aligned} \tag{33}$$

The second term of (32) is

$$E\sum_h \frac{1}{t_h^2}\sum_{\substack{i,r\\ i\neq r}}\psi'_{hi}\psi'_{hr} = \sum_{h,j}\frac{1}{t_h^2}\Big(\sum_i \frac{m_{hij}}{M_{hij}}\psi_{hij}\Big)^2 - \sum_{h,j}\frac{1}{t_h^2}\frac{P_{hj}}{P_h}\sum_i \frac{m^2_{hij}}{M^2_{hij}}\psi^2_{hij} \tag{34}$$

where

$$\psi_{hij} = \sum_k \psi_{hijk};$$

and the third term of (32) is

$$E\sum_{\substack{h,q\\ h\neq q}}\frac{\psi'_h}{t_h}\frac{\psi'_q}{t_q} = \Big[\sum_{h,i,j}\frac{1}{t_h}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\psi_{hij}\Big]^2 - \sum\frac{1}{t_h^2}\Big[\sum_{i,j}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\psi_{hij}\Big]^2. \tag{35}$$

Therefore $EY'^2(r'-r)^2 = (33) + (34) + (35)$, and when $Y_{hijk}(r_{hijk}-r)$ is substituted for ψ_{hijk}, we have

$$\begin{aligned} EY'^2(r'-r)^2 = \sum\frac{1}{t_h^2}\Bigg[&\sum_{i,j}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\frac{M_{hij}-m_{hij}}{M_{hij}-1}\sum Y^2_{hijk}(r_{hijk}-r)^2 \\ &+ \sum_{i,j}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}\frac{m_{hij}-1}{M_{hij}-1}\Big[\sum_k Y_{hijk}(r_{hijk}-r)\Big]^2 \\ &+ \sum_j \frac{P_{hj}}{P_h}\Big[\sum_i \frac{m_{hij}}{M_{hij}}Y_{hij}(r_{hij}-r)\Big]^2 \\ &\quad - \sum_{i,j}\frac{P_{hj}}{P_h}\frac{m^2_{hij}}{M^2_{hij}}Y^2_{hij}(r_{hij}-r)^2 \\ &- \Big\{\sum_{i,j}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}(r_{hij}-r)Y_{hij}\Big\}^2\Bigg] \\ &+ \Big[\sum_{h,i,j}\frac{1}{t_h}\frac{P_{hj}}{P_h}\frac{m_{hij}}{M_{hij}}Y_{hij}(r_{hij}-r)\Big]^2. \end{aligned} \tag{36}$$

By substituting $(r_{hijk} - r_{hij} + r_{hij} - r)^2$ for $(r_{hijk} - r)^2$ in the first term of (36) and $P_{hi}M_{hij}/P_{hij}m_{hij}$ for $1/t_h$ in the 1st, 2nd, and 4th terms, the sum of these three terms becomes

$$\begin{aligned}(37)\qquad &\sum_{h,i,j,k} \frac{P_{hj}}{P_h}\frac{M_{hij}}{m_{hij}}\frac{P_{hi}^2}{P_{hij}^2} F_{hij} Y_{hijk}^2 (r_{hijk} - r_{hij})^2 \\ &+ 2\sum_{h,i,j,k} \frac{P_{hj}}{P_h}\frac{M_{hij}}{m_{hij}}\frac{P_{hi}^2}{P_{hij}^2} F_{hij} Y_{hijk}^2 (r_{hijk} - r_{hij})(r_{hij} - r) \\ &+ \sum_{h,i,j} \frac{P_{hj}}{P_h}\frac{M_{hij}}{m_{hij}}\frac{P_{hi}^2}{P_{hij}^2} F_{hij}(r_{hij} - r)^2 \left[\sum_k Y_{hijk}^2 - \frac{Y_{hij}^2}{M_{hij}}\right]\end{aligned}$$

where $F_{hij} = (M_{hij} - m_{hij})/(M_{hij} - 1)$ and $r_{hij} = \sum_k X_{hijk}/\sum_k Y_{hijk}$.

When we substitute the appropriate value for $1/t_h$ in the 3rd, 5th, and 6th terms of (36), the sum of these terms becomes

$$\begin{aligned}(38)\qquad &\sum_{h,j} \frac{P_{hj}}{P_h}\left[\sum_i \frac{P_{hi}}{P_{hij}} Y_{hij}(r_{hij} - r)\right]^2 - \sum_h \left[\sum_{i,j} \frac{P_{hj}}{P_h}\frac{P_{hi}}{P_{hij}} Y_{hij}(r_{hij} - r)\right]^2 \\ &+ \left[\sum_{h,i,j} \frac{P_{hj}}{P_h}\frac{P_{hi}}{P_{hij}} Y_{hij}(r_{hij} - r)\right]^2.\end{aligned}$$

Now

$$\begin{aligned}(39)\qquad \sum_i \frac{P_{hi}}{P_{hij}} Y_{hij}(r_{hij} - r) &= \sum_i P_{hi}\left(\frac{X_{hij}}{P_{hij}} - \frac{Y_{hij}}{P_{hij}} r\right) = P_h(R_{hj(A)} - rR_{hj(A):Y}) \\ &= P_h R_{hj(A):Y}(\bar{r}_{hj(A)} - r)\end{aligned}$$

where $\bar{r}_{hj(A)} = R_{hj(A)}/R_{hj(A):Y}$, and

$$\begin{aligned}(40)\qquad \sum_{i,j} \frac{P_{hj}}{P_h}\frac{P_{hi}}{P_{hij}} Y_{hij}(r_{hij} - r) &= \sum_j P_{hj}(R_{hj(A)} - rR_{hj(A):Y}) = P_h(R_{h(A)} - rR_{h(A):Y}) \\ &= P_h R_{h(A):Y}(\bar{r}_{h(A)} - r)\end{aligned}$$

where $\bar{r}_{h(A)} = R_{h(A)}/R_{h(A):Y}$.

Substituting (39) and (40) in (38), we have

$$\begin{aligned}(41)\qquad &\sum_{h,j} (P_{hj}/P_h)P_h^2 R_{hj(A):Y}^2(\bar{r}_{hj(A)} - r)^2 - \sum_h P_h^2 R_{h(A):Y}^2(\bar{r}_{h(A)} - r)^2 \\ &+ [\sum_h P_h R_{h(A):Y}(\bar{r}_{h(A)} - r)]^2.\end{aligned}$$

By substituting $(\bar{r}_{hj(A)} - \bar{r}_{h(A)} + \bar{r}_{h(A)} - r)^2$ for $(\bar{r}_{hj(A)} - r)^2$ in the first term in (41) and expanding, (41) becomes

$$\begin{aligned}(42)\qquad &\sum_{h,j} P_h^2 \frac{P_{hj}}{P_h} R_{hj(A):Y}^2(\bar{r}_{hj(A)} - \bar{r}_{h(A)})^2 + 2\sum_{h,j} P_h^2 \frac{P_{hj}}{P_h} R_{hj(A):Y}^2(\bar{r}_{hj(A)} - \bar{r}_{h(A)})(\bar{r}_{h(A)} - r) \\ &+ \sum_h P_h^2(\bar{r}_{h(A)} - r)^2\left[\sum_j \frac{P_{hj}}{P_h} R_{hj(A):Y}^2 - R_{h(A):Y}^2\right] + [\sum_h P_h R_{h(A):Y}(\bar{r}_{h(A)} - r)]^2.\end{aligned}$$

Hence, since $(EY')^2\, E\theta^2 = (37) + (42)$,

$$
\begin{aligned}
(EY')^2 E\theta^2 = {} & \sum_{h,i,j} P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \frac{\sum_k Y_{hijk}^2 (r_{hijk} - r_{hij})^2}{m_{hij} M_{hij} \overline{P}_{hij}^2} \\
& + 2 \sum_{h,i,j} P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \frac{\sum_k Y_{hijk}^2 (r_{hijk} - r_{hij})(r_{hij} - r)}{m_{hij} M_{hij} \overline{P}_{hij}^2} \\
& + \sum_{h,i,j} P_{hi}^2 \frac{P_{hj}}{P_h} \frac{M_{hij} - m_{hij}}{M_{hij} - 1} \sigma_{hij:Y}^2 \frac{(r_{hij} - r)^2}{m_{hij} \overline{P}_{hij}^2} \\
& + \sum_{h,j} P_h^2 (P_{hj}/P_h) R_{hj(A):Y}^2 (\bar{r}_{hj(A)} - \bar{r}_{h(A)})^2 \qquad (43) \\
& + 2 \sum_{h,j} P_h^2 (P_{hj}/P_h) R_{hj(A):Y}^2 (\bar{r}_{hj(A)} - \bar{r}_{h(A)})(\bar{r}_{h(A)} - r) \\
& + \sum_{h,j} P_h^2 (\bar{r}_{h(A)} - r)^2 (P_{hj}/P_h)(R_{hj(A):Y} - R_{h(A):Y})^2 \\
& + [\sum_h P_h R_{h(A):Y} (\bar{r}_{h(A)} - r)]^2
\end{aligned}
$$

where $\sigma_{hij:Y}^2 = \sum_k^{M_{hij}} (Y_{hijk} - \bar{Y}_{hij})^2 / M_{hij}$ and $\bar{Y}_{hij} = \sum_k^{M_{hij}} Y_{hijk}/M_{hij} = Y_{hij}/M_{hij}$.

The approximation to $E(r' - r)^2$ is given by (43) divided by $(EY')^2$. By ignoring the 2nd, 5th, and 7th terms which are negligible for a large class of populations, we obtain (13).

The variance of X' is derived from (43) by simply substituting $\overline{P}_{hij}/P$ for Y_{hijk} in (43). This follows from the considerations given below:

Since $r' = X'/Y'$, and X' is the numerator of r', $\sigma_{X'}^2$ is given by $\sigma_{r'}^2$ when the denominator, Y', is identically equal to unity in repeated samplings.

$$\text{Since } \frac{1}{l_h} = \frac{M_{hij} P_{hi}}{m_{hij} P_{hij}} = \frac{P_{hi}}{m_{hij} \overline{P}_{hij}} \text{ from (5),}$$

the denominator of r' which is equal to

$$\sum_h^L \sum_i^{S_h} \sum_j^1 \sum_k^{m_{hij}} \frac{P_{hi}}{m_{hij} \overline{P}_{hij}} Y_{hijk},$$ will be identically equal to unity in repeated sampling when Y_{hijk} is set equal to $\overline{P}_{hij}/P$ where $P = \Sigma P_h$.

The formula for the mean square error of X' (9), of course is exact since the error term

$$E\{Y'^2/(EY')^2\}\{r' - r\}^2 = 0.$$

It may be pointed out that $\sigma_{X'}^2$ may be obtained directly and more simply without the use of (29) since X' is not estimated from the ratio of random variables.

From (29), the error term for the approximation to $E(r' - r)^2$, $(43)/(EY')^2$, is given by $E\left(1 - \frac{Y'^2}{(EY')^2}\right)\{r' - r\}^2$. This cannot be expressed as a simple func-

tion of the individual observations, but useful maxima and minima for it may be obtained. A method for obtaining the upper and lower bounds of the variance of r' is simply attained from the following inequalities which hold independent of the joint distribution of X' and Y'.

$$\frac{EY'^2}{Y_{\max}^2}(r' - r)^2 \leq E(r' - r)^2 \leq \frac{EY'^2}{Y_{\min}^2}(r' - r)^2 \tag{44}$$

where $Y_{\max}$ is the maximum value of the Y' obtained simply by choosing or estimating the largest Y_h' for each stratum. $Y_{\min}$ (the minimum value of Y') is obtained in a similar manner.

Eq. 44 when evaluated turns out to be

$$\frac{(EY')^2 E\theta^2}{Y_{\max}^2} \leq E(r' - r)^2 \leq \frac{(EY')^2 E\theta^2}{Y_{\min}^2} \tag{45}$$

where $(EY')^2E\theta^2$ is given by (43).

Eq. (45) will serve adequately as an indicator of the accuracy of $E\theta^2$ for sampling systems in which the variability of the Y's within strata is restricted. However, in other designs, where stratification is not used and the variability in the Y's is not restricted the limits given by (45) may be too broad to be useful.

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MULTIPLE SAMPLING WITH CONSTANT PROBABILITY

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1. Introduction. In an attempt to reduce inspection costs, manufacturers have frequently resorted to sampling procedure in which the disposition of an aggregate or lot of similar units does not necessarily depend upon the results of a single sample. In practice, however, the number of permissible additional samples is limited to one or two; nevertheless, if the lot is very large, an appreciable reduction in the expected sample may be accomplished by allowing a greater number of additional samples. In this article probability formulae will be derived for an inspection procedure for infinite lots in which the number of additional samples is not limited and may be any number depending upon the results of the sampling. This development will be limited to the simple case of attribute inspection in which the units fall into two categories—satisfactory units or defective units. If p denotes the fraction defective in an infinite lot, then the probability of finding exactly m defective units or defects in a sample of n is

$$P(m, n) = \binom{n}{m} p^m q^{n-m}, \qquad q = 1 - p. \tag{1}$$

Since $P(m, n)$ is the probability of m successes in n trials with constant probability of success p, though the terminology of commercial inspection will be used in this article, the results are applicable to other situations involving repeated trials with constant probability of success.

In contrast with multiple sampling, a single sample inspection procedure for lots of the type here considered is one in which a lot of units is accepted or rejected on the basis of the number of defective units found in the sample. Thus a lot is accepted if the number of defects is at most an integer c the "acceptance number," and rejected if the number exceeds c. For an infinite lot containing a fraction p of defects and a sample of n units, the probability of accepting is by (1)

$$\prod_{\bullet}(c, n) = \sum_{m \leqq c} P(m, n), \tag{2}$$

and the probability for rejection is the difference between this sum and unity.

2. Multiple sampling. The procedure in multiple sampling is to examine first an initial sample of n_0 units. If the number of defects in this initial sample is at most c the lot is accepted and if the number of defects exceeds $c + k$ (k an integer) the lot is rejected. But if the number of defects is greater than c and less than $c + k + 1$ an additional sample is removed and examined. In the latter case similar criteria determine whether the lot is to be accepted or rejected or this method of sampling continued. With an infinite lot this scheme of samp-

ling has an infinite variety of forms but there are certain advantages in limiting this discussion to the following type of multiple sampling procedure.

I. *Sample Sizes:* The initial sample is of n_0 units but all additional samples are of the same size, namely n units.

II. *Condition for Acceptance:* The lot is accepted if the number of defects in initial sample of n_0 units is at most c or if after taking r additional samples of n the total number of defects in the $n_0 + rn$ units examined equals $c + r$.

III. *Condition for Rejection:* The lot is rejected if the number of defects in initial sample of n_0 units exceeds $c + k$ or if after taking r additional samples of n the total number of defects exceeds $c + r + k$.

IV. *Condition for an Additional Sample:* An additional sample of n is taken only if neither condition II nor condition III is realized.

Thus in this sampling scheme the level for acceptance as well as the level for rejection increases by unity for each additional sample of n. If at the *r-th* additional sample a lot is neither accepted nor rejected then the total number of defects in initial plus additional samples must equal one of the k numbers

$$c + r + 1, c + r + 2, \cdots, c + r + k.$$

Denote the probabilities for obtaining these numbers by

$$P_1(r), P_2(r), \cdots, P_k(r) \tag{3}$$

respectively, the subscript indicating the number of defects in excess of the acceptance level.

To be accepted on the $(r + 1)$-*st* additional sample, (a) no defect must be found in the $(r + 1)$-*st* additional sample and (b) a total of $c + r + 1$ defects must be found in previous samples. The probability of (a) is given by (1), taking m equal to zero, and the probability of (b) is the first one in the set (3). Consequently the probability of accepting a lot on the $(r + 1)$-*st* additional sample is

$$P_0(r + 1) = q^n P_1(r).$$

If Π denotes the probability of eventually accepting the lot

$$\Pi = \sum_{m \leq c} P(m, n_0) + q^n[P_1(0) + P_1(1) + P_1(2) + \cdots], \tag{4}$$

where the first term on the right is the probability of accepting on the initial sample and may be evaluated by means of (1). Furthermore

$$P_i(0) = P(c + i, n_0) \tag{5}$$

and is by (1) the probability of finding $c + i$ defects in initial sample.

According to the notation (3) the probability of finding a total of $c + r + 1 + i$ defects in initial plus $r + 1$ additional samples, that is i more defects than the acceptance level, is $P_i(r + 1)$. These probabilities may be expressed as

linear combinations of the probabilities (3) with coefficients that are probabilities of the type (1). Thus

$$P_i(r+1) = \sum_j P(i-j+1, n)P_j(r) \tag{6}$$

where the sum may be made to extend for $j = 1, 2, \cdots, k$, provided one defines (1) as equal to zero for negative m. By repeated application of this linear transformation it is possible to express the probabilities (3) for additional samples in terms of the probabilities (5) for the initial sample. Thus if M denotes the $k \times k$ square matrix with elements

$$M_{ij} = P(i-j+1, n) \qquad (i, j = 1, \cdots, k), \tag{7}$$

by omitting subscripts and regarding $P(r)$ as a vector with elements given by (3), the linear transformation may be written

$$P(r+1) = MP(r). \tag{8}$$

Hence by repeated application of (8)

$$P(r) = M^r P(0) \qquad (r = 0, 1, 2, \cdots) \tag{9}$$

provided the zero power of the matrix M is defined as the identity matrix I.

The probability $P_i(r)$ cannot exceed the probability of finding exactly $c + r + i$ defects in a single sample of $n_0 + rn$ units, that is, in the notation of (1), the probability $P(c + r + i, n_0 + rn)$. Since the latter probabilities approach zero as r approaches infinity it follows that the limit of the elements of $P(r)$ as r approaches infinity is zero. Thus with this multiple sampling procedure a lot is eventually either accepted or rejected. Furthermore since the matrix M contains no negative elements and $P(0)$ may be chosen with all positive elements it follows that the elements of M^r approach zero as r approaches infinity or

$$\lim_{r\to\infty} M^r = \text{“0”}, \quad \text{the zero matrix.} \tag{10}$$

It can be demonstrated that since the limit (10) is the zero matrix the sum of the infinite geometrical series in the matrix M

$$I + M + M^2 + \cdots = (I - M)^{-1}, \tag{11}$$

where the right member is the reciprocal of the matrix $I - M$. Consequently the infinite sum of vectors

$$V = \sum_{r=0}^{\infty} P(r) = (I - M)^{-1} P(0). \tag{12}$$

This infinite sum of vectors has elements $V_1, V_2, \cdots, V_k$ of which the first element is the sum in brackets occurring in the right member of (4). Hence the probability of eventually accepting the lot

$$\Pi = \sum_{m \leqq c} P(m, n_0) + q^n V_1, \tag{13}$$

and is thus by (12) and (5) expressible in terms of probabilities for the initial sample, equations (1), and the reciprocal of the matrix $I - M$.

In addition to the probability for acceptance one is also interested in the expected number, E, of additional samples. Since

$$\sum_i P_i(r-1) \qquad (r = 1, 2, 3, \cdots),$$

where the sum extends over all $i = 1, 2, \cdots, k$ is the probability of continuing to the r-th sample, it follows that

$$\sum_i P_i(r-1) - \sum_i P_i(r)$$

is the probability that lot will be either accepted or rejected on the r-th sample. Therefore the expected number of additional samples

$$\begin{aligned} E &= \sum_{r>0} r\Big[\sum_i P_i(r-1) - \sum_i P_i(r)\Big] \\ &= \sum_{r\geq 0} \sum_i P_i(r), \end{aligned}$$

or, on interchanging the order of summation and applying (12),

$$E = \sum_i V_i . \tag{14}$$

That is, the expected number of additional samples equals the sum of the elements of the vector V.

Though it is possible to develop a general expression for the reciprocal matrix $I - M$, to determine the acceptance probability, Π, as well as the expected number of additional samples it is only necessary to evaluate V. Now by (12) this vector is the solution of the linear system of equations

$$(I - M)V = P(0). \tag{15}$$

Though for k small this system could be solved directly, in order to find a form of the solution applicable for any value of k, let the expansion in power series in x of

$$[(px + q)^n - x]^{-1} = g_1 + g_2x + g_3x^3 + \cdots , \tag{16}$$

where the coefficients, g, are funetions of p and q. On clearing of fractions and equating coefficients of like powers of x it is found that

$$g_1 = q^{-n} \tag{17}$$

and, by equating the coefficients of the first k powers of x and using the notation (7),

$$g_i - \sum_{j=1\cdots k} M_{ij}g_j = \begin{cases} 0 & (i = 1, 2, \cdots, k-1), \\ g_{k+1} & (i = k). \end{cases} \tag{18}$$

Similarly, if the expansion in power series of

$$\frac{\sum_i P_i(0)x^i}{(px+q)^n - x} = h_1 + h_2 x + h_3 x^3 + \cdots, \tag{19}$$

where the sum is for all $i = 1, \cdots, k$, then by clearing of fractions and equating coefficients of like powers of x it is found that

$$h_1 = 0, \tag{20}$$

and

$$h_i - \sum_{j=1\cdots k} M_{ij} h_j = \begin{cases} -P_i(0) & (i = 1, \cdots, k-1), \\ -P_k(0) + h_{k+1} & (i = k). \end{cases} \tag{21}$$

It follows from equations (18) and (21) that if

$$V_i = g_i h_{k+1}/g_{k+1} - h_i \qquad (i = 1, \cdots, k), \tag{22}$$

then V, the vector with these elements, will satisfy equation (15). Since by (17) and (20)

$$V_1 = q^{-n} h_{k+1}/g_{k+1}, \tag{23}$$

the probability for eventually accepting the lot is by (13) expressible as

$$\Pi = \sum_{m \leq c} P(m, n_0) + h_{k+1}/g_{k+1}, \tag{24}$$

while the expected number of additional samples is the sum of elements (22) of V_i.

These results will now be summarized and simplified formulae derived for special cases. In the summary all probabilities are expressed by means of (5) in terms of the probabilities (1).

3. Summary of multiple sampling formulas. For this multiple sampling procedure the initial sample is n_0 and the additional samples are n. A lot is accepted if on the r-th additional sample the total number of defects found is at most $c + r$ and rejected if the total exceeds $c + r$. An infinite lot containing a fraction p of defects is either accepted or rejected, the probability of acceptance being given by

$$\Pi = \sum_{m \leq c} \binom{n_0}{m} p^m q^{n-m} + h_{k+1}/g_{k+1} \qquad (q = 1 - p), \tag{25}$$

and the probability of rejection is $1 - \Pi$. The expected number of additional samples is

$$E = \frac{h_{k+1}}{g_{k+1}} \sum_i g_i - \sum_i h_i, \tag{26}$$

where the sum extends over $i = 1, 2, \cdots, k$. The g_i and h_i are the coefficients in power series of x in the expansions of:

$$\frac{1}{(px+q)^n - x} = g_1 + g_2 x + g_3 x^2 + \cdots, \tag{27}$$

$$\sum_i \frac{\binom{n_0}{c+i} p^{c+i} q^{n_0-c-i} x^i}{(px+q)^n - x} = h_1 + h_2 x + h_3 x^2 + \cdots, \tag{28}$$

where the sum is for all $i = 1, 2, \cdots, k$. These formulae apply to all finite values of c and k provided the binomial coefficient is zero for values of the argument falling outside those occurring in the ordinary expansion of an integral power of a binomial.

4. Computation of coefficients g and h. If the denominator in (27) is first expanded in power series in

$$x(px+q)^{-n}$$

and then the resulting negative powers of binomials expanded in power series in x, it is found that

$$\begin{aligned} g_1 &= q^{-n}, \\ g_2 &= q^{-2n} - \binom{n}{1} p q^{-n-1}, \\ &\cdots\cdots\cdots\cdots\cdots\cdots \\ g_k &= q^{-kn} - \sum_{m=1,\cdots,k-1} (-1)^{m+1} \binom{(k-m)n+m-1}{m} \\ &\qquad \times p^m q^{-kn+mn-m}, \qquad k \neq 1. \end{aligned} \tag{29}$$

By (28) the coefficients h are expressible in terms of the g's,

$$\begin{aligned} h_1 &= 0, \\ h_k &= \sum_{i=1,\cdots,k-1} \binom{n_0}{c+i} p^{c+i} q^{n_0-c-i} g_{k-i}, \qquad k \neq 1. \end{aligned} \tag{30}$$

Other expressions for the coefficients may be derived from the theory of functions of a complex variable. Thus by Cauchy's Integral Formula

$$\begin{aligned} g_{k+1} &= \frac{1}{2\pi\sqrt{-1}} \int_C \frac{dx}{x^{k+1}[(px+q)^n - x]}, \\ h_{k+1} &= \frac{1}{2\pi\sqrt{-1}} \int_C \frac{S(x)\,dx}{x^{k+1}[(px+q)^n - x]}, \end{aligned} \tag{31}$$

where

$$S(x) = \sum_{i=1,\cdots,k} \binom{n_0}{c+i} p^{c+i} q^{n_0-c-i} x^i, \tag{32}$$

and the closed path of integration C in the complex plane only includes the pole at the origin. Since the integrands are rational functions and the point at infinity is not a singularity for either integrand, these integrals taken about the origin are equal to the negative sum of the corresponding integrals taken about the zeros of

$$(px + q)^n - x.$$

If $p \neq n^{-1}$ it can be demonstrated that there are n distinct zeros $x_1, x_2, \cdots, x_n$ corresponding to the solutions of the algebraic equation

$$(px_s + q)^n = x_s \qquad (s = 1, \cdots, n). \tag{33}$$

One solution is obviously

$$x_1 = 1, \tag{34}$$

and for $p = n^{-1}$ this solution is a double root.

The integrals about these zeros are obtainable from Cauchy's Integral Formula and after integrating and simplifying the resulting sum by means of (33) it is found that for the case $p \neq n^{-1}$,

$$\begin{aligned} g_{k+1} &= \frac{1}{1-np} + \sum_{s=2,\cdots,n} \frac{px_s + q}{x_s^{k+1}[q - (n-1)px_s]}, \\ h_{k+1} &= \frac{S(1)}{1-np} + \sum_{s=2,\cdots,n} \frac{(px_s + q)S(x_s)}{x_s^{k+1}[q - (n-1)px_s]}. \end{aligned} \tag{35}$$

If the power series (27) is multiplied by the series

$$(1-x)^{-1} = 1 + x + x^2 + x^3 + \cdots,$$

the resulting product

$$\frac{1}{(1-x)[(px+q)^n - x]} = g_1 + (g_1 + g_2)x + (g_1 + g_2 + g_3)x^2 + \cdots,$$

so that, by Cauchy's Integral Formula,

$$G_k = \sum_{i=1,\cdots,k} g_i = \frac{1}{2\pi\sqrt{-1}} \int_C \frac{dx}{x^k(1-x)[(px+q)^n - x]}. \tag{36}$$

Similarly the sum of the coefficients h that occur in the right member of (26) may be written

$$H_k = \sum_{i=1,\cdots,k} h_i = \frac{1}{2\pi\sqrt{-1}} \int_C \frac{S(x)\,dx}{x^k(1-x)[(px+q)^n - x]}. \tag{37}$$

The integrals (36) and (37) are of the same type as (31), and by employing the same method of integrating used in deriving (35), the following expressions for the sums of coefficients g and h occurring in (26) are obtained:

$$G_k = \sum_i g_i = \frac{k}{1-np} - \frac{n(n-1)p^2}{2(1-np)^2} + \sum_{s=2,\cdots,n} \frac{px_s + q}{x_s^k(1-x_s)[q-(n-1)px_s]},$$

$$(38)\quad H_k = \sum_i h_i = \frac{kS(1) - S'(1)}{1-np} - \frac{n(n-1)p^2 S(1)}{2(1-np)^2} + \sum_{s=2,\cdots,n} \frac{(px_s+q)S(x_s)}{x_s^k(1-x_s)[q-(n-1)px_s]}$$

provided $np \neq 1$. Here $S'(1)$ is the derivative of (32) with respect to x evaluated for $x = 1$. For the special case $np = 1$, two of the roots of (33)

$$x_1 = x_2 = 1,$$

and the integrals (36), (37) and (38) become respectively

$$(n-1)g_{k+1} = 2kn + \tfrac{8}{3}n - \tfrac{4}{3} + \sum_{s\geq 3} \frac{n + x_s - 1}{x_s^{k+1}(1-x_s)},$$

$$(n-1)h_{k+1} = (2kn + \tfrac{8}{3}n - \tfrac{4}{3})S(1) - 2nS'(1) + \sum_{s\geq 3} \frac{n + x_s - 1}{x_s^{k+1}(1-x_s)} S(x_s),$$

$$(39)\quad (n-1)\sum_i g_i = k^2 n + \tfrac{5}{3}kn + \tfrac{1}{18}n - \tfrac{4}{3}k - \tfrac{1}{18} - \tfrac{1}{9}n^{-1} + \sum_{s\geq 3} \frac{n + x_s - 1}{x_s^k(1-x_s)^2},$$

$$(n-)1\sum_i h_i = (k^2 n + \tfrac{5}{3}kn + \tfrac{1}{18}n - \tfrac{4}{3}k - \tfrac{1}{18} - \tfrac{1}{9}n^{-1})S(1) - (\tfrac{8}{3}n - \tfrac{4}{3} + 2kn)S'(1) + nS''(1) + \sum_{s\geq 3} \frac{n + x_s - 1}{x_s^k(1-x_s)^2} S(x_s),$$

where the sum extends over all roots of (33) that are not equal to unity. Here $S'(1)$ and $S''(1)$ are the first and second derivatives of (32) with respect to x for $x = 1$ and $p = n^{-1}$.

Formulas (35), (38) and (39) require for their evaluation the solutions of equation (33). For n greater than unity there are just two positive real solutions, say $x_1 = 1$ and x_2. If n is even all other roots are complex numbers, while if n is odd they are complex with the exception of one negative real root. Consequently by (33) for $s = 3, 4, \cdots, n$ the absolute values of the roots satisfy the inequality

$$(p \mid x_s \mid + q)^n > x_s,$$

and consequently the $\mid x_s \mid$ cannot be between x_1 and x_2. But equation (33) may be written

$$\frac{(px_s + q)^n - 1}{(px_s + q) - 1} = \frac{1}{p} \qquad (s \neq 1)$$

so that for $s = 2, 3, \cdots, n$

$$\sum_i (px_s + q)^i = 1/p \tag{40}$$

where the sum is taken for $i = 0, 1, \cdots, n-1$ and therefore

$$\sum_i (p\,|\,x_s\,|\, + q)^i > 1/p \qquad (s = 3, 4, \cdots, n).$$

Now x_2 is the only real and positive solution of (40), consequently, in order to satisfy the inequality, the absolute values of roots corresponding to $s = 3, 4, \cdots, n$ must exceed x_2. On combining this result with the former, it follows that

$$|\,x_s\,| > 1 \quad \text{and} \quad x_2. \tag{41}$$

Consequently for large values of k the most important terms in the right members of (35), (38) and (39) correspond to the real positive roots $x_1 = 1$ and x_2 of equation (33). By omitting the terms corresponding to $s = 3, \cdots, n$ one can derive approximations to the g and h and their sums applicable for large k values. In fact for np near unity the roots corresponding to $s = 3, 4, \cdots$ are considerably greater than unity as is illustrated in the following table of roots for the case $np = 1$:

$n = 2, \quad p = 1/2; \quad x_s = 1, 1;$

$n = 3, \quad p = 1/3; \quad x_s = 1, 1, -8;$

$n = 4, \quad p = 1/4; \quad x_s = 1, 1, -7 \pm 4\sqrt{-2};$

$n = 5, \quad p = 1/5; \quad x_s = 1, 1, -12.2531 \cdots,$

$$-4.8734 \cdots \pm 7.7343 \cdots \sqrt{-1}$$

and for $s = 3, 4, 5, \cdots, |\,x_s\,|$ is greater than 8.

For very large values of n and small values of p one can find approximate values for the roots by solving the limit equation obtained from (33) by putting

$$a = np$$

and letting n approach infinity. This equation is

$$e^{a(x_s - 1)} = x_s, \tag{42}$$

where e is the base of the natural logarithms. For the case $a = 1$, the roots are $1, 1, 3.0891 \cdots \pm 7.4602 \cdots \sqrt{-1}$, $3.66 \cdots \pm 13.88 \cdots \sqrt{-1}$ and

$$x_s = \frac{b(1 + \log_e b)}{b^2 + 1}(b - \sqrt{-1}) + b\sqrt{-1} \quad \text{approximately,}$$

where

$$b = (2u + 1/2)\pi, \qquad u = 4, 5, 6, \cdots.$$

From equation (39) and these numerical results it follows that even with k as small as 3 the percentage error for the case $np = 1$ introduced in g_i by omitting the terms in the indicated sum is less than .002%. Consequently for all practical purposes one may omit the complex and negative roots for values of k greater than 3 in computing the g's for np in the neighborhood of unity. For smaller values of k the exact values of the g's are readily obtainable from (29).

5. Special cases. Consider first the case in which $c < 0$ and $n_0 \leqq k + c$. With these conditions, under no circumstances could a lot be accepted or rejected on the initial sample and the indicated sum in the right member of (25) is zero. Furthermore for this case the sum (32) becomes

$$S(x) = (px + q)^{n_0}x^{-c}. \tag{43}$$

Consequently it follows from (33) that

$$S(x_s) = x_s^{t-c}, \tag{44}$$

where

$$t = n_0/n. \tag{45}$$

It should be noted however, that for t not an integer the right member of (44) is multiple valued and one must take that value for which

$$x_s^t = (px_s + q)^{n_0}. \tag{46}$$

Thus for real positive values of x_s, the right member of (44) is real. For integral values of t there is of course no ambiguity in the notation.

If (44) is substituted in the second equation of (35), the resulting expression for the h coefficient is of the same form as that for the g coefficient, in fact

$$h_{k+1} = g_{k-t+c+1},$$

so that by (25) the probability for acceptance is for this case

$$\Pi = g_{k-t+c+1}/g_{k+1}. \tag{47}$$

In similar manner it follows from (43) and (46) that the sum of the h coefficients, equation (38),

$$H_k = G_{k-t+c} + t$$

and hence by (26) the expected number of additional samples

$$E = \Pi G_k - G_{k-t+c} - t. \tag{48}$$

Since the initial sample is nt units and the additional samples are all equal to n units, the expected total number of units, sampled, that is, initial plus additional samples is

$$I = n_0 + nE = n(\Pi G_k - G_{k-t+c}). \tag{49}$$

Since for this case it is impossible to accept or reject on the initial sample one could combine the initial sample with the first additional sample. In fact one can continue combining initial and additional samples and thus increasing c and t provided the new initial sample n_0 and the new c value thus obtained are such that

$$c \leqq 0, \qquad n_0 = nt \leqq k + n - 1 + c. \tag{50}$$

In this process of combining samples t and c increase at the same rate and consequently formula (47), and the right member of (49) are unchanged. In other words formulas (47) and (49) may also be used under conditions (50).

It was demonstrated in Section 3 that for k sufficiently large one can omit those terms in (35) and (38) corresponding to complex or negative roots of (33). If this is done the following useful approximations for the g and G are obtained:

$$\begin{aligned} g_k &= (1 - np)^{-1} + [q - (n-1)px]^{-1} x^{-k+(1/n)}, \\ G_k &= k(1 - np)^{-1} - \tfrac{1}{2}n(n-1)p^2(1 - np)^{-2} \\ &\qquad + [q - (n-1)px]^{-1}(1 - x)^{-1} x^{-k+(1/n)}, \end{aligned} \tag{51}$$

provided $np \neq 1$, $k \neq 1$ and x is the real positive root of

$$(px + q)^n = x \qquad (np \neq 1) \tag{52}$$

that is not equal to unity. For $np = 1$ these approximations become by (39)

$$\begin{aligned} (n-1)g_k &= 2kn + 2n/3 - 4/3 \\ (n-1)G_k &= k^2 n + 5kn/3 + n/18 - 4k/3 - 1/18 - n^{-1}/9, \qquad k \neq 1. \end{aligned} \tag{53}$$

These formulae in conjunction with formulae (47) and (49) give quite satisfactory approximations for the probability for acceptance Π and the expected total number of units sampled even when values of the subscripts employed are as small as 3. Of course the larger the value of k in (51), (52) or (53) the better these approximations.

Now the root x of (52) is greater or less than unity depending on whether the product $a = np$ is less than or greater than unity. Consequently it follows from (47) and (51) that for $c = 0$ and t finite

$$\begin{aligned} \Pi' = \lim_{k\to\infty} \Pi &= \lim_{k\to\infty} g_{k-t+1}/g_{k+1} \\ &= 1, \quad np < 1; \\ &= x^t, \quad np > 1; \end{aligned} \tag{54}$$

while by (49) and (51) the expected total number of units sampled has the limiting value

$$I' = \lim_{k\to\infty} I = \begin{cases} nt(1 - np)^{-1}, & np < 1; \\ \infty, & np > 1. \end{cases} \tag{55}$$

But k infinite implies that under no circumstance can a lot be rejected. Consequently Π' and I' are the exact values of the probability for acceptance and the expected total sample respectively for the following sampling procedure:

The initial sample is $n_0 = nt$ and all additional samples are n. The lot is accepted if on the initial sample no defects are found or if after taking r additional samples a total of exactly r defects is found.

In inspection problems p is usually small and n large so that the approximation (40) may be used to determine the real positive root x, thus

$$e^{a(x-1)} = x \qquad (a = np). \tag{56}$$

It then follows from (54) and (55) that for $np > 1$

$$\begin{aligned} \frac{-\log \Pi'}{1-x} &= n_0 p, \\ \frac{-\log x}{1-x} &= np. \end{aligned} \tag{57}$$

These relations are of course equivalent to (54) and (56). Suppose that the probability Π' and the fraction p are assigned. Then the initial sample n_0, and additional sample n, will depend on only the parameter x. Consider next the problem of sampling a number of lots that fall into two categories, namely those containing a fraction p of defects and those containing a fraction p^* of defects where $p^* < p$. If in addition the sampling procedure is to be such that lots with fraction p^* of defects are eventually accepted, but lots with fraction p of defects have a small assigned probability of acceptance Π', then whatever the value of x as long as the resulting $np \geqq 1$ these conditions are satisfied. Furthermore if one insists that the expected total sample for lots containing a fraction p^*, namely by (55)

$$I'(p^*) = n_0(1 - np^*)^{-1},$$

be a minimum, then it is found that

$$x = p^*/p. \tag{58}$$

This remarkably simple result is capable of still greater generalization. By an altogether different approach to the problem the author has succeeded in proving that of all possible multiple sampling procedures, the multiple sampling method here described and defined by equations (57) and (58) gives the minimum expected inspection for the problem under consideration provided n is sufficiently large.[1]

By letting both $-c$ and k approach infinity it is possible to derive probability formulae for sampling procedure in which a lot is either rejected or the sampling continues without end. These formulae are included in Table I along with other special cases derived from previously listed general formulae.

[1] *Note:* The author has postponed publication of this proof in the hope that it might be generalized to include sampling problems involving both acceptance and rejection of a lot.

TABLE I

Notation:

n = number of units in each additional sample
n_0 = number of units in initial sample
p = fraction defective in lot
$a = np$
$q = 1 - p$
c = maximum number of defects in initial sample for acceptance
$t = n_0/n$ = ratio initial sample to additional samples
$f = c + k + 1$ = minimum number of defects in initial sample for rejection
$c + r$ = number of defects in initial plus first r additional samples for acceptance
$f + r = c + k + 1 + r$ = minimum number of defects in initial plus first r additional samples for rejection
Π = probability of eventually accepting lot with fraction p defects
$1 - \Pi$ = probability of eventually rejecting lot with fraction p defects
I = expected total number of units sampled (i.e., initial plus whatever additional samples are sampled).
x = real positive root different from unity of the equation $(px + q)^n = x$.

Conditions	Π	I
(a) $k = 1$, $c = 0$, $f = 2$	$q^{n_0} \times \dfrac{1 - (n - n_o)\,pq^{n-1}}{1 - npq^{n-1}}$	$n_0 \times \dfrac{1 - (q^{n-1} - q^{n_0-1})np}{1 - npq^{n-1}}$
(b) $k = 1$, $c = 0$, $f = 2$, $n_0 = n$	$q^n(1 - npq^{n-1})^{-1}$	$n(1 - npq^{n-1})^{-1}$
(c) $c = -k$, $f = 1$	q^{n_0-n}/g_{k+1}	$n_0 + nq^{n_0-n}G_k/g_{k+1}$
(d) $k = 1$, $c = -1$, $f = 1$	$q^{n_0+n}(1 - npq^{n-1})^{-1}$	$n_0 + nq^{n_0}(1 - npq^{n-1})^{-1}$
(e) $k = 2$, $e = -2$, $f = 1$	$\dfrac{q^{n_0+2n}}{1 - 2npq^{n-1} + \dfrac{n(n+1)}{2}p^2q^{2n-2}}$	$n_0 + \dfrac{nq^{n_0}(1 + q^n - npq^{n-1})}{1 - 2npq^{n-1} + \dfrac{n(n+1)}{2}p^2q^{2n-2}}$

TABLE I—*Concluded*

Conditions	Π	I
(f) $k = -c$ $= \infty$ $f = 1$	0 for $np > 1$ $q^{n_0-n}(1-np)$ for $np < 1$*	$n_0 + nx(1-x)^{-1}$ for $np > 1$ ∞ for $np < 1$
(g) $c = 0$ $n = 2$ $n_0 = f$ $= k + 1$	$\dfrac{1}{1+(p/q)^{n_0}}$	$\dfrac{n_0(2\Pi - 1)}{q - p}$
(h) $c = 0$ $n = 2$ $n_0 = f$ $= k + 1$ $p = 1/2$	0.5	n_0^2
(i) $c = 0$ $n_0 = n$	g_k/g_{k+1}	$n(\Pi G_k - G_{k-1})$
(j) $c = 0$ $k = \infty$	1 $(np < 1)$ $x^{n_0/n}$ $(np > 1)$	$n_0(1-np)^{-1}$ $(np < 1)$ ∞ $(np > 1)$

* In this sampling procedure a lot cannot be accepted so that Π is the probability that additional samples will be taken without end. The probability of rejecting lot is however $1 - \Pi$.

TABLE II

Values of g and G for Limit $n = \infty$, $p = 0$

$np =$ $a =$	0.2558	0.4024	0.6931	1.0000	1.3863	2.0118	2.5584
$x =$	10	5	2	1	.5	.2	.1
g_1	1.292	1.495	2.000	2.718	4.000	7.477	12.915
g_2	1.338	1.634	2.614	4.671	10.455	40.86	133.76
g_3	1.3432	1.665	2.935	6.667	23.48	208.2	1343.2
g_4	1.3437	1.6717	3.097	8.667	49.55	1045.	13.4×10^3
g_5	1.3438	1.6729	3.178	10.667	101.70	5228.	134×10^3
g_∞	1.3438	1.6732	3.2589	∞	∞	∞	∞
G_1	1.292	1.495	2.000	2.718	4.000	7.477	12.915
G_2	2.629	3.130	4.614	7.389	14.45	48.34	146.7
G_3	3.972	4.795	7.549	14.05	37.93	256.5	1490
G_4	5.316	6.467	10.65	22.72	87.5	1301.	14.9×10^3
G_5	6.660	8.140	13.82	33.39	189.2	6529.	149×10^3

As an illustration of the method of application of these formulae, suppose that the sampling procedure is to be such that the probability, Π, of accepting a "p" value of $0.5 + \epsilon$ equals the probability of rejecting a "p" value of $0.5 - \epsilon$. This condition on probabilities is by Table I, formula (g), always satisfied if $c = 0$, $n = 2$, and $n_0 = k + 1$. This corresponds to a multiple sampling scheme in which additional samples are only two units each and a lot is accepted or rejected on initial sample if none or all units are defective. With $\epsilon = 0.1$ and $\Pi \leqq 1/6$, one can take $n_0 = 4$ and $k = 3$. The expected total number of units examined depends on "p" and varies for this numerical case from 4, for $p = 0$ or 1, to a maximum of 16, for $p = 0.5$. Nevertheless a single sample plan satisfying the same conditions would require a sample of 23 units whatever the value of p.

The previous problem is, however, not typical of those encountered in commercial inspection for in such situations p is usually very small. In practice one can generally replace the formulae in Table I by their limiting values for $n = \infty$, $p = 0$, and $np = a$. Table II gives the limiting values of the g and G as well as x for a small number of values of a.

Finally the justification for multiple sampling lies in the fact that a reduction in the expected total sample is possible. Though this paper is limited to the consideration of a very elementary type of sampling, it indicates that it might be worth while to investigate the possibility of utilizing the methods of multiple sampling in inspection for variables. Unfortunately serious mathematical difficulties are even encountered in so simple a problem as multiple sampling from a normal population for the mean.

AN EXACT TEST FOR RANDOMNESS IN THE NON-PARAMETRIC CASE BASED ON SERIAL CORRELATION[1]

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1. Introduction. A sequence of variates $x_1, \cdots, x_N$ is said to be a random series, or to satisfy the condition of randomness, if $x_1, \cdots, x_N$ are independently distributed with the same distribution; i.e., if the joint cumulative distribution function (c.d.f.) of $x_1, \cdots, x_N$ is given by the product $F(x_1) \cdots F(x_N)$ where $F(x)$ may be any c.d.f.

The problem of testing randomness arises frequently in quality control of manufactured products. Suppose that x in some quality character of a product and that $x_1, x_2, \cdots, x_N$ are the values of x for N consecutive units of the product arranged in some order (usually in the order they were produced). The production process is said to be in a state of statistical control if the sequence $(x_1, \cdots, x_N)$ satisfies the condition of randomness. A number of tests of randomness have been devised for purposes of quality control, all having the following features in common: 1) They are based on runs in the sequence $x_1, \cdots, x_N$. 2) The test procedure is invariant under topologic transformation of the x-axis, i.e., the test procedure leads to the same result if the original variates $x_1, \cdots, x_N$ are replaced by $x_1', \cdots, x_N'$ where $x_\alpha' = f(x_\alpha)$ and $f(t)$ is any continuous and strictly monotonic function of t. 3) The size of the critical region, i.e., the probability of rejecting the hypothesis of randomness when it is true, does not depend on the common c.d.f. $F(x)$ of the variates $x_1, \cdots, x_N$. Condition (3) is *a fortiori* fulfilled if condition (2) is satisfied and if $F(x)$ is continuous. The fulfillment of condition (3) is very desirable, since in many practical applications the form of the c.d.f. $F(x)$ is unknown.

Tests of randomness are of importance also in the analysis of time series (particularly of economic time series) where they are frequently based on the so-called serial correlation. The serial correlation coefficient with lag h is defined by the expression[2] (see, for instance, Anderson [1])

$$R_h = \frac{\sum_{\alpha=1}^{N} x_\alpha x_{h+\alpha} - \left(\sum_{\alpha=1}^{N} x_\alpha\right)^2 \Big/ N}{\sum_{\alpha=1}^{N} x_\alpha^2 - \left(\sum_{\alpha=1}^{N} x_\alpha\right)^2 \Big/ N} \tag{1}$$

where $x_{h+\alpha}$ is to be replaced by $x_{h+\alpha-N}$ for all values of α for which $h + \alpha > N$. The distribution of R_h has recently been studied by R. L. Anderson [1], T. Koopmans [2], L. C. Young [3], J. v. Neumann [4, 5], B. I. Hart and J. v. Neu-

[1] Presented to the Institute of Mathematical Statistics and the American Mathematical Society at a joint meeting at New Brunswick, New Jersey, on September 13, 1943.

[2] Some authors (see, for instance, [2] p. 27, equation (61)) use a non-circular definition

mann [6], and J. D. Williams [7], under the assumption that $x_1, \cdots, x_N$ are independently distributed with the same normal distribution. Thus, in addition to the randomness of the series $(x_1, \cdots, x_N)$ it is assumed that the common c.d.f. of the variates $x_1, \cdots, x_N$ is normal. This is a restrictive assumption since frequently the form of the common c.d.f. $F(x)$ of the variates $x_1, \cdots, x_N$ is unknown.

The purpose of this paper is to develop a test procedure based on R_h such that (*a*) if $F(x)$ is continuous the size of the critical region does not depend on the common c.d.f. $F(x)$ of the variates $x_1, \cdots, x_N$, thus making an exact test of significance possible also when nothing is known about $F(x)$ except its continuity; (*b*) if $F(x)$ is not continuous, but all its moments are finite and its variance is positive, the size of the critical region approaches, as $N \to \infty$, the value it would have if $F(x)$ were continuous. Thus in the limit an exact test is possible in this case as well. We will refer to the case where the form of $F(x)$ is unknown as the non-parametric case, in contrast to the case when it is known that $F(x)$ is a member of a finite parameter family of c.d.f.'s.

The test based on the serial correlation seems to be suitable if the alternative to randomness is the existence of a trend[3] or of some regular cyclical movement in the data. In the analysis of time series it is frequently assumed that this is the case and this is perhaps the reason why tests based on serial correlation are widely used in the analysis of time series. In quality control of manufactured products the existence of a trend is often considered as the alternative to randomness, caused perhaps by the steady deterioration of a machine in the production process. Thus, tests of randomness based on serial correlation could also be used in quality control.

2. An exact test procedure based on R_h. Let a_α be the observed value of $x_\alpha (\alpha = 1, \cdots, N)$. Consider the subpopulation where the set $(x_1, \cdots, x_N)$ is restricted to permutations of $a_1, \cdots, a_N$. In this subpopulation the probability that $(x_1, \cdots, x_N)$ is any particular permutation $(a_1', \cdots, a_N')$ of $(a_1, \cdots, a_N)$ is equal to $1/N!$ if the hypothesis to be tested, i.e., that of randomness, is true. (If two of the a_i $(i = 1, 2, \cdots, N)$ are identical we assume that some distinguishing index is attached to each so that they can then be regarded as distinct and so that there still are $N!$ permutations of the elements $a_1, \cdots, a_N$.)

The probability distribution of R_h in this subpopulation can be determined as follows: Consider the set of $N!$ values of R_h which are obtained by substituting for $(x_1, \cdots, x_N)$ all possible permutations of $(a_1, \cdots, a_N)$. (A value which occurs more than once is counted as many times as it occurs.) Each of these values of R_h has the probability $1/N!$. On the basis of this distribution of R_h an exact test of significance can be carried out. Suppose that α is the level of significance, i.e., the size of the critical region. We choose as critical region a subset of M values out of the set of $N!$ values of R_h where $M/N! = \alpha$. The sub-

[3] If the existence of a trend is feared it may be preferable to use the non-circular statistic discussed, for example, in [2].

set of M values which constitute the critical region will depend in each particular problem on the possible alternatives to randomness. For example, if a linear trend is the only possible alternative to randomness, then the critical region will consist of the M largest values[4] of R_h. The value of the lag h will also be chosen on the basis of the alternatives under consideration. For instance, if some cyclical movement in the data is suspected the choice of h will depend on the form of these cycles. The general idea underlying the choice of the subset of M values and of the lag is to make the power of the test with respect to the alternatives which are particularly feared as high as possible.

If R_h has the same value for several permutations of $(a_1, \cdots, a_N)$, it may be impossible to have a critical region consisting of exactly M values of R_h. For example, if $a_1 = a_2 = \cdots = a_N$, then all the $N!$ values of R_h are equal, and the number of values of R_h included in the critical region must be either 0 or $N!$. If $F(x)$ is continuous the probability that two values of R_h be equal is zero. This explains why an exact test is always possible when $F(x)$ is continuous. On the other hand, if $F(x)$ is not continuous, the probability that several values of R_h be equal is positive. However, the theorem we shall prove in Section 4 shows that in the limit an exact test is possible even when $F(x)$ is not continuous, but has finite moments and a positive variance. For if the latter is true, the probability is one that the weaker conditions for the validity of our theorem (given at the end of Section 4) will be fulfilled.

Consider the statistic

$$\bar{R}_h = \sum_{\alpha=1}^{N} x_\alpha x_{h+\alpha} \tag{2}$$

where $x_{h+\alpha}$ is to be replaced by $x_{h+\alpha-N}$ for all values of α for which $h + \alpha > N$. Since in the subpopulation under consideration $\sum_{\alpha=1}^{N} x_\alpha$ and $\sum_{\alpha=1}^{N} x_\alpha^2$ are constants, the statistic $\bar{R}_h$ is a linear function of R_h in this subpopulation. Hence, the test based on $\bar{R}_h$ is equivalent to the test based on R_h. Since $\bar{R}_h$ is simpler than R_h, in what follows we shall restrict ourselves to the statistic $\bar{R}_h$.

We shall now show that, if h is prime to N, the totality T_h of the $N!$ values taken by $\bar{R}_h$ is the same as T_1, the totality of the $N!$ values taken by $\bar{R}_1$.

In the argument which follows it is to be understood that, whenever a positive integer is greater than N, it is to be replaced by that positive integer less than or equal to N which differs from it by an integral multiple of N.

Clearly it will be sufficient to show the existence of a permutation $p_1, p_2, \cdots, p_N$ of the first N integers such that

$$p_i + 1 = p_{i+h} \qquad (i = 1, 2, \cdots, N).$$

Such a permutation is given by

$$j = p_{(j-1)h+1} \qquad (j = 1, 2, \cdots, N).$$

For if $j \neq j'$ then $(j - 1)h + 1 \not\equiv (j' - 1)h + 1$ because h is prime to N. Hence to every positive integer i there is a unique positive integer j, $(i, j \leq N)$ such

[4] See footnote 3.

that

$$i = (j-1)h + 1$$

Now

$$p_i + 1 = p_{(j-1)h+1} + 1 = j + 1 = p_{jh+1} = p_{i+h},$$

which is the required result.

In what follows we shall restrict ourselves to the case when h is prime to N. This is not a very restrictive assumption since in practice h will be small as compared with N and by omitting a few observations we can always make N prime to h. Since T_h is the same as T_1 we shall deal with the statistic $\bar{R}_1$ only. To simplify the notation we shall write R instead of $\bar{R}_1$. Thus, the test procedure will be based on the statistic

$$R = \sum_{\alpha=1}^{N-1} x_\alpha x_{\alpha+1} + x_N x_1 . \tag{4}$$

If N is very small an exact test of significance can be carried out by actually calculating the $N!$ possible values of R. However, this procedure is practically impossible if N is not small. In Section 3 the exact mean value and variance of R will be calculated, and in section 4 the normality of the limiting distribution of R will be proved. Thus, if N is sufficiently large so that the limiting distribution of R can be used, a test of significance can easily be carried out. Difficulties in carrying out the test arise if N is neither sufficiently small to make the computation of the $N!$ values of R practically possible, nor sufficiently large to permit the use of the limiting distribution. In such cases it may be helpful to determine the third and fourth, and perhaps higher, moments of R, on the basis of which upper and lower limits for the cumulative distribution of R can be derived. (For a description of the Tchebycheff inequalities by which this can be done see, for example, Uspensky, [8], pp. 373–380.) Since the limiting distribution is normal it may be useful to approximate the distribution by a Gram-Charlier series or to employ similar methods.

3. Mean value and variance of R.[5] It is clear that

$$\begin{aligned} E(R) &= NE(x_1 x_2) = \frac{N}{N(N-1)} \sum\sum_{\alpha \neq \beta} a_\alpha a_\beta \\ &= \frac{1}{N-1} [(a_1 + \cdots + a_N)^2 - (a_1^2 + \cdots + a_N^2)]. \end{aligned} \tag{5}$$

To calculate the variance of R we first calculate the second moment of R about the origin. We have

$$\begin{aligned} E(R^2) &= E(x_1x_2 + \cdots + x_{N-1}x_N + x_N x_1)^2 \\ &= NEx_1^2x_2^2 + 2NEx_1x_2^2x_3 + (N^2 - 3N)Ex_1x_2x_3x_4 . \end{aligned} \tag{6}$$

[5] The first four moments of a similar statistic have been obtained by Young [3].

To express the expected values $Ex_1^2x_2^2$, $Ex_1x_2^2x_3$, and $Ex_1x_2x_3x_4$ we shall introduce the following notations for the symmetric functions of $a_1, \cdots, a_N$: For any set of positive integers $i_1, i_2, \cdots, i_k$ the symbol $S_{i_1 i_2 \cdots i_k}$ denotes the symmetric function $\sum_{\alpha_k} \cdots \sum_{\alpha_1} a_{\alpha_1}^{i_1} \cdots a_{\alpha_k}^{i_k}$ where the summation is to be taken over all possible sets of k positive integers $\alpha_1, \cdots, \alpha_k$ subject to the restriction that $\alpha_u \leq N$ and $\alpha_u \neq \alpha_v$ $(u, v = 1, \cdots, k)$.

From (6) we easily obtain

$$E(R^2) = \frac{N}{N(N-1)} S_{22} + \frac{2N}{N(N-1)(N-2)} S_{121} + \frac{N^2 - 3N}{N(N-1)(N-2)(N-3)} S_{1111} \tag{7}$$

$$= \frac{S_{22}}{(N-1)} + \frac{2S_{121}}{(N-1)(N-2)} + \frac{S_{1111}}{(N-1)(N-2)}.$$

It will probably facilitate computation to express each of the symmetric functions in the right member of (7) by a sum of terms, each a product of factors $S_r (r = 1, 2, \cdots)$. One can easily verify the relationships

$$S_{11} = S_1^2 - S_2 \tag{8}$$

$$S_{12} = S_{21} = S_1S_2 - S_3 \tag{9}$$

$$S_{13} = S_{31} = S_1S_3 - S_4 \tag{10}$$

$$S_{22} = S_2^2 - S_4 \tag{11}$$

$$S_{111} = S_{11}S_1 - 2S_{12} = (S_1^2 - S_2)S_1 - 2(S_1S_2 - S_3) \tag{12}$$

$$= S_1^3 - 3S_1S_2 + 2S_3$$

$$S_{112} = S_{121} = S_{211} = S_{11}S_2 - 2S_{13} \tag{13}$$

$$= (S_1^2 - S_2)S_2 - 2(S_1S_3 - S_4)$$

$$= S_1^2S_2 - S_2^2 - 2S_1S_3 + 2S_4$$

$$S_{1111} = S_{111}S_1 - 3S_{112} \tag{14}$$

$$= S_1^4 - 3S_1^2S_2 + 2S_1S_3 - 3S_1^2S_2 + 3S_2^2 + 6S_1S_3 - 6S_4$$

$$= S_1^4 - 6S_1^2S_2 + 8S_1S_3 + 3S_2^2 - 6S_4.$$

It follows from (5) that

$$E(R) = \frac{1}{N-1}(S_1^2 - S_2), \tag{15}$$

and from (7), (11), (13), (14), and (15) that the variance of R is given by

$$\sigma^2(R) = E(R^2) - [E(R)]^2$$

$$= \frac{S_2^2 - S_4}{N-1} + \frac{S_1^4 - 4S_1^2S_2 + 4S_1S_3 + S_2^2 - 2S_4}{(N-1)(N-2)} - \frac{1}{(N-1)^2}(S_1^2 - S_2)^2. \tag{16}$$

The mean value and variance of R can easily be computed from (15) and (16) as soon as the values of S_1, S_2, S_3, and S_4 have been determined.

The formulas (15) and (16) are considerably simplified if $S_1 = 0$. In the special case that $S_1 = 0$ we have

$$E(R) = -\frac{S_2}{N-1} \tag{15'}$$

and

$$\sigma^2(R) = \frac{S_2^2 - S_4}{N-1} + \frac{S_2^2 - 2S_4}{(N-1)(N-2)} - \frac{S_2^2}{(N-1)^2}. \tag{16'}$$

We can always make S_1 equal to zero by replacing a_α by $b_\alpha = a_\alpha - N^{-1}\Sigma a_\alpha$. This substitution is permissible, since it changes the statistic R only by an additive constant and consequently leaves the test procedure unaffected. Thus, in practical applications it may be convenient to replace a_α by b_α and to use formulas (15') and (16').

4. Limiting distribution of R. Let $\{a_\alpha\}$ ($\alpha = 1, 2, \cdots$ ad inf.) be a sequence of real numbers with the following properties:

a) There exists a sequence of numbers $A_1, A_2, \cdots, A_r, \cdots$ such that

$$\frac{1}{N}\left|\sum_{\alpha=1}^{N} a_\alpha^r\right| \leq A_r \qquad (r = 1, 2, \cdots \text{ ad inf.}) \tag{17}$$

for all N. (This condition means that the moments about the origin of the sequence $a_1, a_2, \cdots, a_N$ are bounded functions of N.)

b) If

$$\delta(N) = \frac{1}{N}\left[\sum_{\alpha=1}^{N} a_\alpha^2 - \frac{1}{N}\left(\sum_{\alpha=1}^{N} a_\alpha\right)^2\right],$$

then

$$\liminf_N \delta(N) > 0. \tag{18}$$

(This condition means that the dispersion of the N values $a_1, a_2, \cdots, a_N$ is eventually bounded below.)

Let $R(N)$ be the serial correlation coefficient R as defined in (4), where $x_1, \cdots, x_N$ is a random permutation of $a_1, a_2, \cdots, a_N$. We shall prove the following

THEOREM: *As $N \to \infty$, the probability that*

$$\frac{R(N) - E(R(N))}{\sigma(R(N))} < t$$

approaches the limit

$$\frac{1}{\sqrt{2\pi}}\int_{-\infty}^{t} e^{-\frac{1}{2}x^2}\,dx.$$

For any function $f(N)$ and any positive function $\phi(N)$ let

$$f(N) = O(\phi(N))$$

mean that $|f(N)/\phi(N)|$ is bounded from above for all N, and let

$$f(N) = \Omega(\phi(N))$$

mean that

$$f(N) = O(\phi(N))$$

and that $\liminf_N |f(N)/\phi(N)| > 0$. Also let

$$f(N) = o(\varphi(N))$$

mean that

$$\lim_{N\to\infty} \frac{f(N)}{\phi(N)} = 0.$$

Let $[\rho]$ denote the largest integer less than or equal to ρ.

To simplify the proof we shall temporarily assume:

c) There exists a positive constant K such that, for every positive integral N,

$$-K \leq S_1 = \sum_{\alpha=1}^{N} a_\alpha \leq K. \tag{19}$$

This restriction will be removed later.

LEMMA 1:

$$\sum_{\alpha_1<\cdots<\alpha_k} \cdots \sum a_{\alpha_1} a_{\alpha_2} \cdots a_{\alpha_k} = O(N^{[\frac{1}{2}k]}).$$

PROOF: $\sum_{\alpha_1<\cdots<\alpha_k} \cdots \sum a_{\alpha_1} \cdots a_{\alpha_k}$ can be written as the sum of a finite number of terms where each term is a product of factors S_r $(r = 1, 2, \cdots)$. This representation will be called the normal representation of $\sum \cdots \sum a_{\alpha_1} \cdots a_{\alpha_k}$. Since $S_1 = O(1)$ by (19) and $S_r = O(N)$ by (17) and since the number of factors S_r $(r > 1)$ in a single term of the normal representation of $\sum \cdots \sum a_{\alpha_1} \cdots a_{\alpha_k}$ is at most $[\frac{1}{2}k]$, the equation $\sum \cdots \sum a_{\alpha_1} \cdots a_{\alpha_k} = O(N^{[\frac{1}{2}k]})$ must hold.

LEMMA 2: *Let* $y = x_1 \cdots x_k z$, *where* $z = x_{k+1}^{i_1} \cdots x_{k+r}^{i_r}$ *and* $i_j > 1$ $(j = 1, \cdots, r)$. *If* $(x_1, \cdots, x_N)$ *is a random permutation of* $a_1, \cdots, a_N$, *and if* $k, r, i_1, \cdots, i_r$ *are fixed values independent of* N, *then* $E(y) = O(N^{[\frac{1}{2}k]-k})$.

PROOF: Let $E(y \mid x_{k+1}, \cdots, x_{k+r})$ be the conditional expected value of y when $x_{k+1}, \cdots, x_{k+r}$ are fixed. It follows easily from Lemma 1 that

$$E(y \mid x_{k+1}, \cdots, x_{k+r}) = O(N^{[\frac{1}{2}k]-k}).$$

Hence also $E(y) = O(N^{[\frac{1}{2}k]-k})$ and Lemma 2 is proved.

Denote $x_\alpha x_{\alpha+1}$ by $y_\alpha (\alpha = 1, \cdots, N-1)$ and $x_N x_1$ by y_N, and consider the expansion of $(y_1 + \cdots + y_N)^r$. Let y be a term of this expansion, i.e., $y = \frac{N!}{i_1! \cdots i_u!} y_{\alpha_1}^{i_1} \cdots y_{\alpha_u}^{i_u}$ $(\alpha_1 < \alpha_2 < \cdots < \alpha_u)$. We will say that two factors y_α and y_β are neighbors if $|\alpha - \beta + 1|$ or $|\alpha - \beta - 1|$ is either 0 or N. The set of u factors $y_{\alpha_1}, \cdots, y_{\alpha_u}$ can be subdivided into cycles as follows: The first cycle contains y_{α_1} and all those y_α which can be reached from y_{α_1} by a succession of neighboring y_α. The second cycle contains the first y_α of the remaining sequence and all those which can be reached from the first y_α by a succession of neighboring y_α. The third cycle is similarly constructed from the remaining sequence, etc. After a finite number of cycles have been withdrawn the sequence will be exhausted. If m is the number of such cycles we will say that y has m cycles.

LEMMA 3: *Let y be a term of the expansion $(x_1x_2 + \cdots + x_Nx_1)^r = (y_1 + \cdots + y_N)^r$ (r fixed). Let m be the number of cycles in y and k be the number of linear factors in y if y is written as a function of $x_1, \cdots, x_N$ (i.e., if we replace y_α by $x_\alpha x_{\alpha+1}$). Then the maximum value of $m + [\frac{1}{2}k] - k$ is equal to $[\frac{1}{2}r]$.*

PROOF: First we maximize $m + [\frac{1}{2}k] - k$ with respect to k when m is fixed. If $m \leq [\frac{1}{2}r]$, then the minimum value of k is obviously zero. Let $m = [\frac{1}{2}r] + r'$ $(r' > 0)$. The minimum value of k is reached if each cycle consists of a single factor y_α and if each factor y_α in y is either linear or squared. If r is even, then the minimum value of k is $4r'$ and if r is odd then the minimum value of k is $4r' - 2$. Hence for $m = [\frac{1}{2}r] + r'$ we have

$$\max_k (m + [\tfrac{1}{2}k] - k) = [\tfrac{1}{2}r] - r' \qquad \text{if } r \text{ is even}$$

and

$$= [\tfrac{1}{2}r] - r' + 1 \text{ if } r \text{ is odd.}$$

Hence maximizing with respect to m and k we obtain

$$\max (m + [\tfrac{1}{2}k] - k) = [\tfrac{1}{2}r],$$

and Lemma 3 is proved.

LEMMA 4: *The expected value of the sum of all those terms in the expansion of $(x_1x_2 + \cdots + x_Nx_1)^r$ for which m is the number of cycles and k the number of linear factors (if y is expressed in terms of $x_1, \cdots, x_N$) is equal to $O(N^{m+[\frac{1}{2}k]-k})$.*

This Lemma follows from Lemma 2 and the fact that the number of terms y with the required properties is $O(N^m)$.

LEMMA 5:

$$E(x_1x_2 + \cdots + x_Nx_1)^r = O(N^{[\frac{1}{2}r]}).$$

This follows from Lemmas 3 and 4.

LEMMA 6: *If r is even then*

$$E(x_1x_2 + \cdots + x_Nx_1)^r = \left(C_{\frac{1}{2}r}^N \left(\frac{r!}{2^{\frac{1}{2}r}}\right) E(x_1^2 x_2^2 \cdots x_r^2)\right) + o(N^{\frac{1}{2}r}).$$

PROOF: It follows easily from our considerations in proving Lemma 3 that $m + [\frac{1}{2}k] - k < \frac{1}{2}r$ for all terms in the expansion of $(x_1x_2 + \cdots + x_Nx_1)^r$ which are not of the type $x_1^2 \cdots x_r^2$. Hence it follows from Lemma 4 that the expected value of the sum of all those terms in the expansion of $[x_1x_2 + \cdots + x_Nx_1]^r$ which are not of the type $x_1^2 \cdots x_r^2$ is equal to $o(N^{\frac{1}{2}r})$. Lemma 6 follows from the fact that $2^{-\frac{1}{2}r}r!$ is the coefficient of the terms of the type $x_1^2 \cdots x_r^2$ in the expansion of $(x_1x_2 + \cdots + x_Nx_1)^r$ and that the number of terms of such type is equal to $C_{\frac{1}{2}r}^N$.

LEMMA 7. $\lim_{N\to\infty} \dfrac{E(x_1x_2 + \cdots + x_Nx_1)^r}{\{E(x_1x_2 + \cdots + x_Nx_1)^2\}^{\frac{1}{2}r}} = 0$ *if* r *is odd and* $= 2^{-\frac{1}{2}r}r!/(\frac{1}{2}r)!$ *if* r *is even.*

PROOF: From Lemma 6 it follows that

$$E(x_1x_2 + \cdots + x_Nx_1)^2 = NE(x_1^2x_2^2) + o(N) = \Omega(N). \tag{20}$$

The first half of Lemma 7 follows from Lemma 5 and equation (20). If r is even then it follows from (20) that

$$\begin{aligned} \lim \frac{E(x_1x_2 + \cdots + x_Nx_1)^r}{\{E(x_1x_2 + \cdots + x_Nx_1)^2\}^{\frac{1}{2}r}} &= \lim_{N\to\infty} \frac{2^{-\frac{1}{2}r}C_{\frac{1}{2}r}^N r!\, E(x_1^2 \cdots x_r^2)}{N^{\frac{1}{2}r}(Ex_1^2x_2^2)^{\frac{1}{2}r}} \\ &= \lim \frac{r!}{2^{\frac{1}{2}r}(\frac{1}{2}r)!} \frac{E(x_1^2 \cdots x_r^2)}{(E(x_1^2x_2^2))^{\frac{1}{2}r}}. \end{aligned} \tag{21}$$

It follows from (17), (19), and the normal representation of symmetric functions that

$$k! \sum_{a_{\alpha_1} < a_{\alpha_2} < \cdots < a_{\alpha_k}} \cdots \sum a_{\alpha_1}^2 \cdots a_{\alpha_k}^2 = S_2^k + O(N^{k-1}).$$

From (17) and (18) we have $S_2 = \Omega(N)$. Since

$$E(x_1^2 \cdots x_r^2) = r!\Big(\sum_{a_{\alpha_1} < a_{\alpha_2} < \cdots < a_{\alpha_r}} \cdots \sum a_{\alpha_1}^2 \cdots a_{\alpha_r}^2\Big)[N(N-1) \cdots (N-r+1)]^{-1},$$

we obtain

$$\lim_{N\to\infty} \frac{E(x_1^2 \cdots x_r^2)}{(E(x_1^2x_2^2))^{\frac{1}{2}r}} = 1. \tag{22}$$

The second half of Lemma 7 follows from (21) and (22).

LEMMA 8:

$$\lim_{N\to\infty} \frac{E(R(N))}{\sigma(R(N))} = 0, \tag{23}$$

$$\lim_{N\to\infty} \frac{E(R^2(N))}{\sigma^2(R(N))} = 1. \tag{24}$$

PROOF: Equation (24) is a trivial consequence of (23). From (15) $E(R) = O(1)$ and from (16) $\sigma(R) = \Omega(N^{\frac{1}{2}})$. The lemma follows easily from these relations.

PROOF OF THE THEOREM: According to Lemma 7 the r-th moment of $R[E(R^2)]^{-\frac{1}{2}}$ approaches the r-th moment of the normal distribution as $N \to \infty$. From this and Lemma 8 the required result follows if condition (c) holds. It remains therefore merely to remove condition (c). Assume now only that $a_1, a_2, \cdots, a_\alpha, \cdots$ satisfy conditions (a) and (b).

$R(N)$ is formed from the population of values $a_1, a_2, \cdots, a_N$. Addition of a constant q to $a_1, \cdots, a_N$ adds the same constant to all the values of $R(N)$ and hence leaves $[R(N) - E(R(N))]/\sigma(R(N))$ unaltered. Let $q^{(N)}$ be $-\sum_{\alpha=1}^{N} a_\alpha/N$ and write $b_\alpha^{(N)} = a_\alpha + q^{(N)}$. Consider the sequences

$$B^{(i)} = b_1^{(i)}, b_2^{(i)}, \cdots, b_i^{(i)} \qquad (i = 1, 2, \cdots, \text{ad inf.}).$$

From (17) it follows that the $| q^{(N)} |$ are bounded for all N. Hence the sequences $B^{(i)}$ satisfy condition (a). They obviously satisfy condition (c). Since $\delta(j)$ is invariant under addition of a constant we have

$$\liminf_j \frac{1}{j}\left(\sum_{\alpha=1}^{j} (b_\alpha^{(j)})^2 - \frac{1}{j}\left(\sum_{\alpha=1}^{j} b_\alpha^{(j)}\right)^2\right) > 0,$$

so that the $B^{(i)}$ satisfy condition (b). Since $[R(N) - E(R(N))]/\sigma(R(N))$ has the same distribution in the sequence $a_1, a_2, \cdots, a_N$ as in the sequence $B^{(N)}$, the theorem follows.

It should be remarked that the theorem remains valid if conditions (a) and (b) are replaced by the weaker condition

$$\mu_r/\mu_2^{\frac{1}{2}r} = O(1) \qquad (r = 3, 4, \cdots, \text{ad inf.})$$

where

$$\mu_r = \frac{1}{N}\sum_{\alpha=1}^{N}\left(a_\alpha - \frac{1}{N}\sum_{\alpha=1}^{N} a_\alpha\right)^r.$$

This follows easily from the fact that $[R(N) - E(R(N))]/\sigma(R(N))$ remains unaltered if we replace the sequence $a_1, \cdots, a_N$ by the sequence $c_1^N, c_2^N, \cdots, c_N^N$ where

$$c_\alpha^N = \left(a_\alpha - \frac{1}{N}\sum_{1}^{N} a_\alpha\right) \Big/ \left[\frac{1}{N}\Sigma\left(a_\alpha - \frac{1}{N}\Sigma\, a_\alpha\right)^2\right]^{\frac{1}{2}}.$$

Conditions (a) and (b) are obviously satisfied by the sequence $c_1^N, \cdots, c_N^N$.

5. Transformation of the original observations.

Let $f(t)$ be a continuous and strictly monotonic function of t $(-\infty < t < +\infty)$. Suppose we replace the original observations $a_1, \cdots, a_N$ by $d_1, \cdots, d_N$, where $d_\alpha = f(a_\alpha)$ $(\alpha = 1, \cdots, N)$. We obtain a valid test of significance if we carry out the test procedure as if $d_1, \cdots, d_N$ were the observed values instead of $a_1, \cdots, a_N$. We could also replace the observed values $a_1, \cdots, a_N$ by their ranks. The question arises whether there is any advantage in making the test on the transformed values instead of on the original observations. It may well

be that by certain transformations we could considerably increase the power of the test with respect to alternatives under consideration. This problem needs further study.

6. Summary. A test procedure based on serial correlation is given for testing the hypothesis that $x_1, \cdots, x_N$ are independent observations from the same population, i.e., that $x_1, \cdots, x_N$ is a random series. By considering the distribution of the serial correlation coefficient in the subpopulation consisting of all permutations of the actually observed values a test procedure is obtained such that

a) if the common c.d.f. $F(x)$ is continuous, the size of the critical region, i.e., the probability of rejecting the hypothesis of randomness when it is true, does not depend upon $F(x)$,

b) if $F(x)$ is not continuous but all its moments are finite and its variance is positive, the size of the critical region approaches, as $N \to \infty$, the value it would have if $F(x)$ were continuous. Thus in the limit an exact test is possible in this case as well.

It is shown that the test based on the serial correlation with lag h is equivalent to the test based on the statistic[6]

$$\sum_{\alpha=1}^{N} x_\alpha x_{h+\alpha}$$

where $x_{h+\alpha}$ is to be replaced by $x_{h+\alpha-N}$ for all values of α for which $h + \alpha > N$. If h is prime to N, the distribution of $\sum_1^N x_\alpha x_{h+\alpha}$ is exactly the same as the distribution of $R = \sum_1^N x_\alpha x_{1+\alpha}$.

The mean value and variance of R are given by the following expressions:

$$E(R) = (S_1^2 - S_2)/(N - 1)$$

and

$$\sigma^2(R) = \frac{S_2^2 - S_4}{N-1} + \frac{S_1^4 - 4S_1^2S_2 + 4S_1S_3 + S_2^2 - 2S_4}{(N-1)(N-2)} - \frac{(S_1^2 - S_2)^2}{(N-1)^2}$$

where $S_r = x_1^r + \cdots + x_N^r$.

It is shown that under some mild restrictions the limiting distribution of R is normal. The test procedure can therefore be easily carried out when N is sufficiently large to permit the use of the limiting distribution of R.

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ON A GENERAL CLASS OF "CONTAGIOUS" DISTRIBUTIONS

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1. Introduction. In a paper of considerable interest, J. Neyman [11] recently discussed frequently occurring situations where the usual tests of significance fail. He discussed, in particular, experiences in entomology and bacteriology which cannot be described by the usual distribution functions and he constructed several new types of apparently contagious distributions. Now at first glance Neyman's investigation may seem of a rather specialized nature, and his distributions of a restricted applicability. It may therefore be useful to point out that they are intimately related to results obtained by various authors in connection with topics having so little apparent relation as accident statistics, telephone traffic, fire damage, sickness- and life-insurance, risk theory, and even an engineering problem. Viewed in the proper light of a general theory, Neyman's method is particularly closely related to some too little known considerations by Greenwood and Yule [6]. These authors were the first to find, and apply, the distribution which shortly afterwards was independently rediscovered by Eggenberger and Polya[1] [3, 4].

Greenwood and Yule discussed two types of what may conveniently be called contagion: with one type there is *true contagion* in the sense of Polya and Eggenberger, where each "favorable" event increases (or decreases) the probability of future favorable events; with the second type the events are, strictly speaking, independent and an *apparent contagion* is actually due to an inhomogeneity of the population. The two explanations are very different in nature as well as in practical implications. It is therefore most remarkable that Greenwood and Yule found their distribution assuming an *apparent contagion*; in their opinion this distribution *contradicts* true contagion. On the contrary, Polya and Eggenberger arrived at the *same* distribution assuming *true* contagion, while the possibility of an apparent contagion due to inhomogeneity seems not to have been noticed by them. The Greenwood-Yule-Polya-Eggenberger distribution has found many applications.[2] Therefore the possibility of its interpretation in two ways, diametrically opposite in their nature as well as in their implications is of greatest statistical significance. This fact is, incidentally, a justification for general theories in statistics.

We shall see that Neyman's contagious distributions belong to the *second* type and are related to the Polya-Eggenberger distribution only if the latter is

[1] The fact that the Polya-Eggenberger distribution is identical with the Greenwood-Yule distribution seems to be mentioned in the literature only in a Stockholm thesis by O. Lundberg [9].

[2] Of quite recent applications we mention Kitagawa and Huruya [8], Rosenblatt [15], O. Lundberg [9]. Only the latter seems aware of the double nature of the distribution.

interpreted in the sense of Greenwood and Yule. In Neyman's case as well as in the other cases referred to above we are concerned with inhomogeneous populations and there exists an extremely simple device to describe such situations appropriately. Once stated, this device will appear trivial. Nevertheless, a straightforward application of it would have avoided considerable mathematical difficulties in the literature and, occasionally, yielded better and simpler results. It seems also the simplest description of the mechanism behind many observed distributions, and therefore suited for a theory of tests[3].

To start in a purely formal manner, consider an arbitrary cumulative distribution function (c.d.f.) $F(x, a)$, depending on a parameter a, and another c.d.f. $U(a)$. *Then*

$$G(x) = \int F(x, a)\, dU(a) \tag{1.1}$$

(the integration extending over the domain of variation of a) *is again a c.d.f.* If, in particular, $U(a)$ is a step function, (1.1) reduces to

$$G(x) = \Sigma p_i F(x, a_i), \tag{1.2}$$

where p_i is the weight attached to a_i (we have, of course, $p_i \geq 0$, $\Sigma p_i = 1$). Instead of (1.2) one can write more simply

$$G(x) = \Sigma p_i F_i(x), \tag{1.3}$$

where the $F_i(x)$ are arbitrary c.d.f.'s. Of course, $F(x, a)$ and $U(a)$ may depend on additional parameters, and the procedure can be repeated.

The statistical meaning of (1.3) is clear. Consider a population made up of several subgroups $A_1, A_2, \cdots$, mixed at random in proportions $p_1 : p_2 : \cdots$. If $F_i(x)$ is the c.d.f. of some character in A_i, then $G(x)$, as defined by (1.3), will represent the c.d.f. of that character in the total population, provided that the subgroups A_i are statistically independent. Similarly (1.1) describes an infinitely composite population. Postponing a discussion of the property of contagion to the last section, we shall first deduce a few properties of the *compound Poisson-distribution*, considered first by Greenwood and Yule. Neyman's "Contagious Distributions of Type A" as well as the Polya-Eggenberger distribution belong to this class. Our next example of a special case of (1.1) is what F. E. Satterthwaite [16] called the "Generalized Poisson Distribution." It has been independently discovered by many authors and represents heterogeneity of quite different a nature. Instead of further examples we shall, in the fourth section, show how Neyman's most general contagious distribution can be deduced by a repeated application of (1.1).

[3] Incidentally, attention may be drawn to an argument by Greenwood and Yule showing that the χ^2-test when applied to the Poisson distribution is biased and tends to exaggerate the goodness of fit. The argument could be amplified from other experience.

Notation: If $F(x)$ and $G(x)$ are the c.d.f.'s of two independent variates X and Y, then their *convolution*, (that is to say the c.d.f. of $X + Y$) will be denoted by $F(x)*G(x)$. Thus

$$F(x)*G(x) = \int_{-\infty}^{+\infty} F(x - y)\, dG(y). \tag{1.4}$$

More particularly we shall write

$$F(x)*F(x) = F^{2*}(x), \tag{1.5}$$
$$F^{n*}(x)*F(x) = F^{(n+1)*}(x).$$

We shall denote by $E(x)$ the *unitary c.d.f.*

$$E(x) = \begin{cases} 0 & \text{for } x < 1, \\ 1 & \text{for } x \geq 1, \end{cases} \tag{1.6}$$

so that $E^{n*}(x) = 0$ for $x < n$, and 1 for $x \geq n$.

2. The compound Poisson distribution. Consider the well-known Poisson expression

$$\pi(n; a) = e^{-a}\frac{a^n}{n!}, \tag{2.1}$$

where the parameter $a > 0$ gives the expected number of "events". We shall refer to (2.1) as the *simple Poisson distribution*. If different individuals of a population are associated with different values of a, and if the character a is distributed according to the cumulative probability law $U(a)$, the probability of n events in the total population will be given by

$$\pi_n = \int_0^\infty e^{-a}\frac{a^n}{n!}\, dU(a). \tag{2.2}$$

Following Greenwood and Yule we shall refer to (2.2) as the *compound Poisson distribution*. Referring for an interpretation to the last section, we first consider a few special cases.

a) If $U(a)$ is a step function we are led to expressions of the form

$$\pi_n = \frac{1}{n!}\sum_i p_i e^{-a_i} a_i^n. \tag{2.3}$$

Such a distribution has been successfully applied by C. Palm [12] to problems of telephone traffic, and by O. Lundberg [9] to sickness statistics.

b) If $U(a)$ is a Pearson Type III distribution

$$U'(a) = \left(\frac{1}{d}\right)^{\frac{h}{d}} \frac{1}{\Gamma\left(\frac{h}{d}\right)} e^{\frac{-a}{d}} a^{\frac{a}{d}-1} \tag{2.4}$$

(with $d > 0, h > 0$), then

$$\pi_n = \frac{1}{n!} \frac{\Gamma\left(n + \frac{h}{d}\right)}{\Gamma\left(\frac{h}{d}\right)} (1 + d)^{-\frac{d}{h}} \left(\frac{1}{1 + d}\right)^n. \tag{2.5}$$

This is the *Polya-Eggenberger distribution* in its usual form, and has in this form (with a slight change of notations) been derived by Greenwood and Yule.

c) If a takes on the values kc only, where $c > 0$ is a constant and $k = 0, 1, \cdots$, and if a is distributed according to the Poisson law

$$Prob\ \{a = kc\} = e^{-\lambda} \frac{\lambda^k}{k!}, \tag{2.6}$$

then

$$\pi_n = e^{-\lambda} \frac{c^n}{n!} \sum_{k=0}^{\infty} \frac{k^n}{k!} (e^{-c}\lambda)^k. \tag{2.7}$$

This is Neyman's *contagious distribution of type A* depending on two parameters (cf. section 4). If, instead, a is distributed according to a multiple Poisson law of form (2.3) we arrive at Neyman's *more-parametric distribution of type A*. They are, of course, essentially linear combinations of expressions of form (2.7).

It follows from the theory of Laplace transforms that *two compound Poisson distributions associated with different c.d.f.'s $U(a)$ are never identical.*

The compound Poisson distribution gives a simple explanation of a phenomenon recorded by Neyman and observable in many instances. In the experiments described by Neyman "the attempts to fit the Poisson Law $\cdots$ failed almost invariably with the characteristic feature that, as compared with the Poisson Law, there were too many empty plots and too few plots with only one larva". It is easily checked in the literature that similar situations arise frequently. Now the Poisson distribution is usually fitted by the method of moments. Accordingly, the compound Poisson law (2.2) ought to be compared with the simple Poisson distribution with the same mean value. The mean value of (2.2) is

$$m = \int_0^{\infty} a\, dU(a), \tag{2.8}$$

so that (2.2) ought to be compared with the Poisson distribution $\pi(n; m)$. Now, *whatever the c.d.f. $U(a)$, we have always*

$$\pi_0 \geq \pi(0, m) \tag{2.9}$$

and

$$\frac{\pi_1}{\pi_0} \leq m = \frac{\pi(1, m)}{\pi(0, m)}. \tag{2.10}$$

As a matter of fact, using Lagrange's form for the remainder in Taylor's formula, we have

$$\begin{aligned} \pi_0 &= e^{-m} \int_0^\infty e^{m-a}\, dU(a) \\ &\geq e^{-m} \int_0^\infty \{1 + (m - a)\}\, dU(a) = e^{-m} = \pi(0, m), \end{aligned} \tag{2.11}$$

which proves (2.9). Similarly

$$\begin{aligned} m\pi_0 - \pi_1 &= e^{-m} \int_0^\infty e^{m-a}(m - a)\, dU(a) \\ &\geq e^{-m} \int_0^\infty (m - a)\, dU(a) = 0, \end{aligned} \tag{2.12}$$

which proves (2.10).

The above theorem shows that, *whenever the material under observation is not quite homogeneous so that the compound Poisson law applies instead of the simple one, there will be too many cases with "no event" and, as compared with these cases, too few with "one event".* It should be noticed, however, that it is *not* strictly true that *always*

$$\pi_1 < \pi(1, m). \tag{2.13}$$

As a matter of fact, even in the numerical example given by Neyman, the computed value π_1 exactly equals the observed value. Still, the inequality (2.13) will hold whenever the third moment about the mean of $U(a)$ is smaller than twice the second. Writing

$$\begin{aligned} \sigma^2 &= \int_0^\infty (a - m)^2\, dU(a), \\ M &= \int_0^\infty (a - m)^3\, dU(a), \end{aligned} \tag{2.14}$$

and using two more terms in the Taylor development of e^{m-a} than in (2.11) and (2.12) we see that

$$\pi_0 \geq e^{-m}\left\{1 + \frac{\sigma^2}{2} - \frac{1}{6}M\right\} \tag{2.15}$$

and

$$m\pi_0 - \pi_1 \geq e^{-m}\{\sigma^2 - \tfrac{1}{2}M\}. \tag{2.16}$$

These inequalities are slightly sharper than (2.9) and (2.10), and often permit us to estimate the variance of $U(a)$.

We note furthermore that the *variance of the compound Poisson distribution is*

$$\sigma^2 + m \tag{2.17}$$

as compared with the variance m of the corresponding simple Poisson distribution. Finally the following important property of the compound distribution may be mentioned: *Consider two independent variates X and Y distributed according to two compound Poisson distributions* $\{\pi_n^{(1)}\}$ *and* $\{\pi_n^{(2)}\}$ *associated with the c.d.f.'s* $U_1(a)$ *and* $U_2(a)$, *respectively. Then the variate* $X + Y$ *is distributed according to a compound Poisson law* $\{\pi_n\}$ *associated with the c.d.f.* $U(a) = U_1(a) * U_2(a)$ (cf. (1.4)).

It suffices to note that $U_i(a) \equiv 0$ for $a < 0$, so that

$$U(a) = \int_0^a U_1(a - s)\, dU_2(s);$$

therefore, after a permitted change of the order of integration

$$\begin{aligned}
\pi_n &= \int_0^\infty e^{-a} \frac{a^n}{n!}\, dU(a) \\
&= \int_0^\infty dU_2(s) \int_s^\infty e^{-a} \frac{a^n}{n!}\, dU_1(a - s) \\
&= \int_0^\infty dU_2(s) \int_0^\infty e^{-(s+t)} \frac{(s + t)^n}{n!}\, dU_1(t) \\
&= \sum_{k=0}^{n} \frac{1}{k!} \frac{1}{(n - k)!} \pi_k^{(1)} \pi_{n-k}^{(2)};
\end{aligned}$$

the last expression represents the convolution of $\{\pi_n^{(1)}\}$ and $\{\pi_n^{(2)}\}$.

Neyman's distributions of type A with two parameters are special cases of a compound Poisson process where $U(a)$ is a step function with jumps at equidistant places, the jumps being given by a simple Poisson distribution $\{\pi(n; \lambda)\}$. Now the convolution of two such distributions is again a simple Poisson distribution $\{\pi(n; 2\lambda)\}$ with jumps at the same places; hence the convolution of two distributions of type A is again a similar distribution with one parameter doubled.

As mentioned before, the notion of a compound Poisson distribution is due to Greenwood and Yule [6]. The time dependent compound Poisson process has been the object of detailed investigations by J. Dubourdieu [2] and O. Lundberg [9]. The latter has discussed also the problem of fitting the compound Poisson process to empirical distributions.

3. The generalized Poisson distribution. Let $F(x)$ be an arbitrary c.d.f. Then its n-fold convolution $F^{n*}(x)$ (cf. (1.5)) may be considered as a c.d.f. depending on a parameter n. Choosing, for the latter, the simple Poisson distribution (2.1) and performing the operation indicated in (1.1), we arrive at the c.d.f. of *the generalized Poisson law*

$$G(x) = \sum_{n=0}^{\infty} e^{-a} \frac{a^n}{n!} F^{n*}(x). \tag{3.1}$$

If, in particular, $F(x)$ is the unitary function (1.6), we have the ordinary Poisson law

$$\prod(x) = \sum_{n=0}^{\infty} e^{-a}\frac{a^n}{n!}E^{n*}(x) = \sum_{n=0}^{[x]} e^{-a}\frac{a^n}{n!} \tag{3.2}$$

in its cumulative form.

The most frequently encountered application of the generalized Poisson distribution is to problems of the following type. Consider independent random events for which the simple Poisson distribution may be assumed, such as: telephone calls, the occurrence of claims in an insurance company, fire accidents, sickness, and the like. With each event there may be associated a random variable X. Thus, in the above examples, X may represent the length of the ensuing conversation, the sum under risk, the damage, the cost (or length) of hospitalization, respectively. To mention an interesting example of a different type, A. Einstein Jr. [5] and G. Polya [13, 14] have studied a problem arising out of engineering practice connected with the building of dams, where the events consist of the motions of a stone at the bottom of a river; the variable X is the distance through which the stone moves down the river.

Now, if $F(x)$ is the c.d.f. of the variable X associated with a single event, *then* $F^{n*}(x)$ is the c.d.f. of the accumulated variable associated with n events. Hence (3.1) is the probability law of the sum of the variables (sum of the conversation times, total sum paid by the company, total damage, total distance travelled by the stone, etc.).

In view of the above examples, it is not surprising that the law (3.1), or special cases of it, have been discovered, by various means and sometimes under disguised forms, by many authors. Quite recently Satterthwaite [16] was led to it (in the above simple form) from problems in insurance. Related (but less elegant) considerations may be found in a paper by W. G. Ackermann [1]. Simple as they are, the above considerations leading to (3.1) furnish a complete solution of the problem in all the cases mentioned. Unfortunately, the special features of the problems often so overshadow the essential point, that one is often led to unnecessarily complicated and incomplete solutions. As an example of the difficulties in considering special cases we mention that Polya [13, 14] was led to a partial differential equation of the hyperbolic type, which conceals the elementary nature of the problem.

If $F(x)$ is itself a Poisson c.d.f. (3.1) reduces to (2.7). *Thus Neyman's distribution of type A depending on two parameters is both a compound and a generalized Poisson distribution.* We shall later on see that the generalized Poisson distribution plays an even more important rôle in Neyman's theory.

The main properties of (3.1) are easily derived using characteristic functions. If $\varphi(z)$ is the characteristic function of $F(x)$, the characteristic function of $G(x)$ is

$$\psi(z) = e^{a(\varphi(z)-1)}. \tag{3.3}$$

Accordingly *the r-th semi-invariant of $G(x)$ equals the r-th moment of $F(x)$ multiplied by a^{-1}*. Moreover it is readily seen that *the r-th convolution of $G(x)$ with itself is again a function of type* (3.1), *only with a replaced by ra*. Neyman's Proposition II is a special case of this remark.

4. Neyman's contagious distributions. As an illustration of the general applicability of the operation (1.1) we shall consider the typical example treated by Neyman. Consider the distribution of larvae in a field. The field is divided into plots of equal areas and we are interested in the probability c_k that exactly k larvae are found in a certain plot. Now we assume with Neyman:

(*i*) The larvae may come from various litters. It is assumed that the probability that exactly ν litters are represented on our plot is given by the simple Poisson distribution[4] (2.1). (*ii*) The probability that there are exactly n survivors is the same for all litters and will be denoted by $p(n)$. (*iii*) If, in any particular litter, there are exactly n survivors, the probability that k of them are found on the plot under observation is given by the *binomial distribution*. We shall write the latter in its cumulative form

$$B(x, n, u) = \sum_{k=0}^{n} \binom{n}{k} u^k (1-u)^{n-k} E^{k*}(x), \tag{4.1}$$

(cf. (1.6)). (*iv*) The parameter u in (4.1) is characteristic for any particular litter (and varies, in particular, with the position of the litter relative to the particular plot under observation). The c.d.f. of u (which characterizes the distribution of litters in the field) is supposed to be known and will be denoted by $F(u)$. The litters are statistically independent.

Now for any particular litter the probability that at most k survivors will be in the plot under observation is given by

$$L(k, u) = \sum_{n=0}^{\infty} p(n) B(k, n, u), \tag{4.2}$$

which is a special case of (1.2). Here u is the parameter for the litter picked out. Accordingly, the probability that at most k survivors from any one litter will be found on our plot is

$$L(k) = \int_0^1 L(k, u)\, dF(u), \tag{4.3}$$

and this is the second application of the operation (1.1). Since any number of litters may be represented on our plot, the final expression for the probability

[4] Actually Neyman at first assumes the number of litters in the field to be finite and considers therefore the binomial instead of the Poisson distribution. Later, however, a passage to the limit is performed which is equivalent to the above assumption. It will be seen that in the following consideration the Poisson distribution may be replaced by any other distribution.

that at most k larvae will be found on our plot is obtained in the form of a *generalized Poisson c.d.f.*

$$C(k) = \sum_{n=0}^{\infty} e^{-a} \frac{a^n}{n!} L^{n*}(k). \tag{4.4}$$

This is the desired c.d.f. For the desired probability c_k we have $c_k = C(k) - C(k-1)$.

We specialize now with Neyman the assumption (*ii*) to the effect that the distribution function $\{p(n)\}$ is a Poisson distribution

$$p(n) = e^{-\lambda} \frac{\lambda^n}{n!}. \tag{4.5}$$

The distribution (4.2) then becomes the c.d.f. of a generalized Poisson distribution, since $B(x, n, u) = B^{n*}(x, 1, u)$.

The simplest special case arises when all litters are characterized by the same value of the parameter, say $u = u_0$. Then $F(u) = E\left(\frac{x}{u_0}\right)$, and $L(k) = L(k, u_0)$. Writing $L'(k) = L(k) - L(k-1)$ for the probability that exactly k survivors from any one litter will be found on our plot, we have

$$\begin{aligned} L'(k) &= \sum_{n=k}^{\infty} e^{-\lambda} \frac{\lambda^n}{n!} \binom{n}{k} u_0^k (1-u_0)^{n-k} \\ &= e^{-\lambda u_0} \frac{(\lambda u_0)^k}{k!}. \end{aligned} \tag{4.6}$$

The c.d.f. (4.4) then reduces to the form (2.7). Similarly, when $F(u)$ is a step function we arrive at Neyman's more parametric distributions of type A.

If $F(u) = u$ for $0 < u < 1$ (rectangular distribution), then $\int_0^1 B(k, n, u)\, dF(u)$ has only jumps of magnitude $1/(n+1)$, and

$$L'(k) = \sum_{n=k}^{\infty} \frac{e^{-\lambda} \lambda^n}{(n+1)!}. \tag{4.7}$$

This leads to Neyman's function of type B. The characteristic function of (4.7) is readily seen to be

$$l(z) = \frac{1}{\lambda} \frac{e^{\lambda(e^{iz}-1)} - 1}{e^{iz} - 1},$$

so that the characteristic function of the final c.d.f. $C(k)$ becomes

$$\exp\left\{a\left(\frac{1}{\lambda} \frac{e^{\lambda(e^{iz}-1)} - 1}{e^{iz} - 1} - 1\right)\right\},$$

in agreement with Neyman's formula.

5. The nature of contagion. It is well known that the simple Poisson distribution describes mutually independent events; in other words, with a Poisson distribution the numbers of events in two non-overlapping time intervals are uncorrelated and the occurrence of an event has no influence on the probability of occurrence of further events. Accordingly, the compound Poisson process also applies to independent and *not* contagious events. With really contagious events (as, for example, with epidemics) the occurrence of each event increases (or decreases) the probability of further events. Greenwood and Yule [6] developed a very general scheme for such events but, due to the very generality, their formulas became too complex for practical applications. They considered the compound Poisson process, and, in particular, the Polya distribution (2.5), as an alternative hypothesis. Accordingly, they interpreted the good fit of that distribution to accident statistics as indicating that there was *no* contagion but that proneness to accidents varies with the person.

Considering a very similar problem, Polya and Eggenberger were later on led to consider a special model of true contagion. This turns out to be the simplest case of the general Greenwood-Yule scheme, but this had been overlooked by them. Curiously enough, Polya was led exactly to the distribution (2.5) which Greenwood and Yule found as an alternative to contagion. It is therefore seen that, contrary to a wide-spread opinion, *an excellent fit of Polya's distribution to observations is not necessarily indicative of any phenomenon of contagion in the mechanism behind the observed distribution.* In order to decide whether or not there is contagion, it is not sufficient to consider the distribution of events, but a detailed study of the correlation between various time intervals is necessary.[5]

The double interpretation of Polya's distribution leads to an understanding of the compound Poisson distribution. To the observer *the compound Poisson distribution will always appear "contagious"; however, this contagion is not inherent in any phenomenon in nature, but simply in our method of sampling.* As a matter of fact, with a compound Poisson distribution the parameter a is a random variable.[6] Its a priori c.d.f. in the total population is $Prob\ \{a \leq x\} = U(x)$. Now if, for any particular sample, the observed number of events is n, then the a posteriori c.d.f. of a *in that sample* is given by

$$Prob\ \{a \leq x\} = \frac{\int_0^x e^{-s} \frac{s^n}{n!}\, dU(s)}{\int_0^\infty e^{-s} \frac{s^n}{n!}\, dU(s)}.$$

[5] For such studies cf. Newbold [10] and Lundberg [9]. For some generalizations of the Polya-Eggenberger scheme see Kitagawa [17] and Rosenblatt [15].

[6] It will be noticed that here a is actually a random characteristic in the population and can be sampled. We are therefore not guilty of the absurdity which is usually connected with the unfortunate use of Bayes' theorem, when a constant is regarded as random variable. If the output of a machine is distributed according to a Poisson distribution, its parameter is a constant, characteristic of that machine. Regarding it as a random variable means to consider the collective of non-existing similar machines and making predictions for them, whereas we are interested in the one machine only.

This is additional information enabling us to make better predictions for the future or estimates of other properties of the sample. For example, if n is very large, there is a considerable probability that the mean of a in the sample exceeds that of the total population: accordingly, we shall expect that also in the future the number of events in our sample will be comparatively large. In other words, although the events themselves are strictly independent we have an apparent contagion due to our method of observation.

It is hardly necessary to point out that the contagion studied by Neyman is of the type just described. Any inhomogeneity of a population of type (1.1) will lead to such an apparent contagion. However, that the Polya-Eggenberger distribution is a member of our class of contagious distributions must be regarded as accident and due to the possibility of its being interpreted as a compound Poisson distribution.

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ON THE CONSTRUCTION OF SETS OF ORTHOGONAL LATIN SQUARES[1]

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1. Introduction.

An m-sided Latin square is an arrangement of m symbols into a square in such a way that no row and no column contains any symbol twice. Two Latin squares are called orthogonal if, when one is superimposed upon the other, every pair of symbols occurs only once. For instance the squares

$$\begin{array}{ccc} A & B & C \\ B & C & A \\ C & A & B \end{array} \qquad \begin{array}{ccc} \alpha & \beta & \gamma \\ \gamma & \alpha & \beta \\ \beta & \gamma & \alpha \end{array}$$

are orthogonal. The resulting square is

$$\begin{array}{ccc} A\alpha & B\beta & C\gamma \\ B\gamma & C\alpha & A\beta \\ C\beta & A\gamma & B\alpha. \end{array}$$

A pair of orthogonal Latin squares is called a Graeco-Latin square. A method has not yet been found by which all possible sets of mutually orthogonal squares can be constructed. However, methods are available for constructing certain special sets, and although we cannot obtain all possible sets with these methods they yield a great variety of designs.

To understand these methods we shall have to use certain fundamental concepts of the theory of numbers. In the following we shall deal therefore only with integers and all symbols used will denote only integers.

Let a, b, m denote certain integers. We say

$$a \equiv b \ (m),$$

(in words a is congruent to b modulo m) if $a - b$ is divisible by m.

Such congruences can be treated like equations. For instance: If $a \equiv b \ (m)$, then $a \pm c \equiv b \pm c \ (m)$, $ac \equiv bc \ (m)$. The proofs of these statements are obvious from the definition of $a \equiv b \ (m)$.

If $a \equiv b \ (m)$, *and* $c \equiv d \ (m)$, *then* $ac \equiv bd \ (m)$, *and* $a \pm c \equiv b \pm d \ (m)$.

PROOF: According to our definition we have

$$a - b = \lambda_1 m \qquad a = b + \lambda_1 m$$

$$c - d = \lambda_2 m \qquad c = d + \lambda_2 m$$

[1] An expository paper presented, at the invitation of the program committee, on September 12, 1943 at the Sixth Summer Meeting of the Institute, at the New Jersey College for Women, Rutgers University, New Brunswick, N. J.

$ac = bd + m(\lambda_2 b + \lambda_1 d + \lambda_1\lambda_2 m)$ and $a \pm c = b \pm d + m(\lambda_1 - \lambda_2)$. Hence $ac - bd$ and $(a \pm c) - (b \pm d)$ are divisible by m.

We have to be more careful with the division of congruences but we shall prove the following rule.

If a is prime to m and $ab \equiv ac$ (m) then $b \equiv c$ (m).

PROOF: $a(b - c) = \lambda_1 m$, by hypothesis. The left side of this equation is divisible by m. Since a is prime to m, $b - c$ must be divisible by m.

This rule means that we may cancel as in an ordinary equation as long as the cancelled factor is prime to the modulus.

Every number is congruent to one of the numbers $0, 1, 2, \cdots, m - 1$, because if a is any number we can find a number b such that $0 \leq a - bm = j < m$.

We shall now add, subtract and multiply mod m. That means we add, subtract and multiply in the ordinary way but shall always replace every number by its smallest positive remainder. Thus for instance

$$2 + 4 \equiv 1 \ (5)$$

$$2 \cdot 4 \equiv 3 \ (5).$$

2. Complete sets of m-sided orthogonal Latin squares, where m is prime. Now let p be a prime number. We write down the following design

$$\begin{array}{cccc} 0 & 1 & \cdots & p-1 \\ j & 1+j & \cdots & p-1+j \\ 2j & 1+2j & \cdots & p-1+2j \\ \vdots & \vdots & \vdots & \vdots \\ (p-1)j & 1+(p-1)j & \cdots & p-1+(p-1)j \end{array} = L_j; \quad 0 < j \leq p-1$$

where all expressions are to be taken mod p, that is we replace every number in this square by its smallest remainder mod p. We shall show that L_j is a Latin square. Here the rows and columns are numbered from 0 to $p - 1$. Assume that the kth row $(0 \leq k \leq p - 1)$ contains a number twice. Then we would have

$$a + kj \equiv b + kj \ (p) \qquad \text{with } a \not\equiv b \ (m).$$

But from this we obtain $a \equiv b$ (p), which is a contradiction. Now assume that a column contains a number twice. Then we would have

$$a + kj \equiv a + k'j \ (p), \qquad \text{with } k \not\equiv k' \ (m)$$

but from this we have

$$kj \equiv k'j \ (p),$$

and since j is prime to p

$$k \equiv k' \ (p),$$

which is again a contradiction.

We can obtain $p-1$ such Latin squares corresponding to the $p-1$ values which j can take.

We shall show that L_i is orthogonal to L_j if $i \neq j$. If this were not true we would have the same pair of numbers occurring in two different boxes of the square which results from the superimposition of L_i on L_j. Let mn be such a pair and assume that it occurs in the αth row and βth column and the γth row and δth column of the resulting square. Then m would occur in L_j in the αth row and βth column and in the γth row and δth column. Hence we would have

$$\beta + \alpha j \equiv m \equiv \delta + \gamma j \ (p), \tag{i}$$

and similarly

$$\beta + \alpha i \equiv n \equiv \delta + \gamma i \ (p). \tag{i'}$$

If we subtract the second congruence from the first we obtain

$$\alpha(j - i) \equiv \gamma(j - i) \ (p),$$

but $j < p$ and $i < p$ and $j \neq i$. Hence $j - i \not\equiv 0 \ (p)$ and we may therefore divide by $(j - i)$. This gives

$$\alpha \equiv \gamma \ (p).$$

Substituting this in (i) we obtain

$$\beta \equiv \delta \ (p).$$

Hence the two boxes must be the same. We have therefore the following theorem:

THEOREM 1: *If p is a prime number and*

$$L_j = \begin{matrix} 0 & 1 & \cdots & p-1 \\ j & 1+j & \cdots & p-1+j \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ (p-1)j & 1+(p-1)j & \cdots & p-1+(p-1)j \end{matrix}$$

then $L_1, L_2, \cdots, L_{p-1}$ is a set of $p-1$ orthogonal Latin squares.

As an application we can write down a set of 4 orthogonal Latin squares of side 5

L_1	L_2	L_3	L_4
0 1 2 3 4	0 1 2 3 4	0 1 2 3 4	0 1 2 3 4
1 2 3 4 0	2 3 4 0 1	3 4 0 1 2	4 0 1 2 3
2 3 4 0 1	4 0 1 2 3	1 2 3 4 0	3 4 0 1 2
3 4 0 1 2	1 2 3 4 0	4 0 1 2 3	2 3 4 0 1
4 0 1 2 3	3 4 0 1 2	2 3 4 0 1	1 2 3 4 0

A further simplification can be achieved if we know a primitive root mod p. A primitive root is a remainder a mod p such that every other remainder except 0

is equal to a power of a mod p. For example, 3 is a primitive root mod 7, for $3^0 \equiv 1\ (7)$, $3^1 \equiv 3(7)$, $3^2 \equiv 2(7)$, $3^3 \equiv 6(7)$, $3^4 \equiv 4(7)$, $3^5 \equiv 5(7)$.

For any number a we must have $a^{p-1} \equiv 1\ (p)$. We will prove this equation for primitive roots only, since we do not need the general case. Let a be a primitive root and assume that

$$a^{p-1} \equiv b \equiv a^q\ (p), \qquad \text{with } q < p-1.$$

Then we would have

$$a^{p-1-q} \equiv a^{p'} \equiv 1\ (p), \qquad \text{with } p' < p-1.$$

Hence we can obtain at most $p-2$ different remainders $a^0 a^1, \cdots, a^{p'-1}$ and a would not be a primitive root.

We now form

$$\bar{L}_i = \begin{matrix} 0 & 1 & \cdots & p-1 \\ a^{0+i} & 1+a^{0+i} & \cdots & p-1+a^{0+i} \\ a^{1+i} & 1+a^{1+i} & \cdots & p-1+a^{1+i} \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ a^{p-2+i} & 1+a^{p-2+i} & \cdots & p-1+a^{p-2+i} \end{matrix} \cdot \quad (i = 0, 1, \cdots, p-2)$$

Exactly as in the case of the L_j of Theorem 1 it can be shown that $\bar{L}_i$ is orthogonal to $\bar{L}_j$ if $i \neq j$. For $k < p-1$ the k-th row of $\bar{L}_i$ equals the $(k-1)$st row of $\bar{L}_{i+1}$ and since $a^{p-1} \equiv 1\ (p)$ the last row of $\bar{L}_{i+1}$ equals the first row of $\bar{L}_i$. Hence $\bar{L}_{i+1}$ is obtained from $\bar{L}_i$ by a cyclical permutation of the $(p-1)$ last rows. It is then only necessary to construct the first square. The others can be obtained by a cyclic permutation of the $(p-1)$ last rows. We shall exemplify this by constructing a set of 6 seven-sided orthogonal squares.

L_1

0 1 2 3 4 5 6
1 2 3 4 5 6 0
3 4 5 6 0 1 2
2 3 4 5 6 0 1
6 0 1 2 3 4 5
4 5 6 0 1 2 3
5 6 0 1 2 3 4

L_2

0 1 2 3 4 5 6
3 4 5 6 0 1 2
2 3 4 5 6 0 1
6 0 1 2 3 4 5
4 5 6 0 1 2 3
5 6 0 1 2 3 4
1 2 3 4 5 6 0

L_3

0 1 2 3 4 5 6
2 3 4 5 6 0 1
6 0 1 2 3 4 5
4 5 6 0 1 2 3
5 6 0 1 2 3 4
1 2 3 4 5 6 0
3 4 5 6 0 1 2

L_4

0 1 2 3 4 5 6
6 0 1 2 3 4 5
4 5 6 0 1 2 3
5 6 0 1 2 3 4
1 2 3 4 5 6 0
3 4 5 6 0 1 2
2 3 4 5 6 0 1

L_5

0 1 2 3 4 5 6
4 5 6 0 1 2 3
5 6 0 1 2 3 4
1 2 3 4 5 6 0
3 4 5 6 0 1 2
2 3 4 5 6 0 1
6 0 1 2 3 4 5

L_6

0 1 2 3 4 5 6
5 6 0 1 2 3 4
1 2 3 4 5 6 0
3 4 5 6 0 1 2
2 3 4 5 6 0 1
6 0 1 2 3 4 5
4 5 6 0 1 2 3

In the theory of numbers it is shown that a primitive root exists for every prime number. If p is not too large a primitive root can easily be found by trial and error. We give a list of primitive roots for all primes under 30:

Prime number	Primitive root
3	2
5	2
7	3
11	2
13	2
17	3
19	2
23	5
29	2

In computing the first row of the first square it is not necessary to actually compute all powers of the primitive root. We can take advantage of the fact that a congruence may be multiplied by a number. Thus, for instance, for the first row of the 11-sided square we have $2^0 \equiv 1\ (11)$ $2^1 \equiv 2\ (11)$ $2^2 \equiv 4\ (11)$ $2^3 \equiv 8\ (11)$ $2^4 \equiv 5\ (11)$ $2^5 \equiv 2.5 \equiv 10\ (11)$ but $10 \equiv -1\ (11)$, hence we have without further computation $2^6 \equiv -2 \equiv 9\ (11)$ $2^7 \equiv -4 \equiv 7\ (11)$ $2^8 \equiv -8 \equiv 3\ (11)$ $2^9 \equiv -5 \equiv 6\ (11)$.

3. Complete sets of m-sided orthogonal Latin squares, where m is the power of a prime.

We have seen that we can always construct $m - 1$ orthogonal Latin squares if m is a prime number. We shall show how to construct $m - 1$ orthogonal Latin squares if m is the power of a prime. However, if we need only a Graeco-Latin square of side m and if m is odd, then we can use the following theorem:

THEOREM 2: *If m is odd, then the squares*

$$L_1 = \begin{array}{cccc} 0 & 1 & \cdots & m-1 \\ 1 & 1+1 & \cdots & m-1+1 \\ 2 & 1+2 & \cdots & m-1+2 \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ m-1 & 1+m-1 & \cdots & m-1+m-1 \end{array}$$

$$L_2 = \begin{array}{cccc} 0 & 1 & \cdots & m-1 \\ 2 & 1+2 & \cdots & m-1+2 \\ 2.2 & 1+2.2 & \cdots & m-1+2.2 \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ 2(m-1) & 1+2(m-1) & \cdots & m-1+2(m-1) \end{array}$$

are orthogonal.

The proof is similar to the proof of Theorem 1. We have to use the fact that 2 is prime to m.

We shall now prove the following statement: *For every remainder* $a \not\equiv 0(p)$ *there exists another remainder* a^{-1} *such that* $a \cdot a^{-1} \equiv 1(p)$.

PROOF: We form the sequence $a, a^2, \cdots, a^n, \cdots$. Since there is only a finite number of remainders, there must exist 2 values i and j such that

$$a^i \equiv a^j(p)$$

Let $i > j$. Then since a is prime to p we may divide by a^j. Putting $i - j = d$, we obtain

$$a^{i-j} = a^d \equiv 1(p).$$

Hence we may take $a^{-1} = a^{d-1}$ and our statement is proved. Thus we see that the system of remainders mod p with respect to addition as well as with respect to multiplication if 0 is excluded satisfies the following postulates:

(1) For every pair of elements A, B there is defined a product $A \cdot B$ within the system such that for any 3 elements A, B and C

$$A \cdot (B \cdot C) = (A \cdot B) \cdot C \qquad \text{(associative law)}$$

The "multiplication" may be any sort of composition. For example, either addition or multiplication of remainder classes.

(2) There exists a unit element 1 such that

$$A \cdot 1 = 1 \cdot A = A.$$

(3) For every A in the system there exists an element A^{-1} such that

$$A \cdot A^{-1} = A^{-1} \cdot A = 1.$$

The unit element will be 0 if we consider the remainder classes with addition as composition. It will be 1 if multiplication is the composition. The inverse of a is $-a$ for the additive system, a^{-1} for the multiplicative system.

A system satisfying (1), (2) and (3) is called a group. The property $A \cdot B = B \cdot A$ is usually not postulated. If a group fulfills this condition, then it is called a commutative group or an Abelian group. A group can be defined by its generating elements. For example, let G be generated by the elements P, Q with the relations $P^2 = 1, Q^3 = 1$ and $PQ = Q^2P$. We then obtain the elements of G as $1, P, Q, PQ, PQ^2, Q^2$. The rules for the multiplication can be written down in the form of a table:

1	P	Q	PQ	PQ^2	Q^2
P	1	PQ	Q	Q^2	PQ^2
Q	PQ^2	Q^2	P	PQ	1
PQ	Q^2	PQ^2	1	Q	P
PQ^2	Q	P	Q^2	1	PQ
Q^2	PQ	1	PQ^2	P	Q

By inspection one can see that taking the elements of our group as symbols the multiplication table forms a Latin square. For instance, if we identify P with 2, Q with 3, etc. we obtain from the table above

1	2	3	4	5	6
2	1	4	3	6	5
3	5	6	2	4	1
4	6	5	1	3	2
5	3	2	6	1	4
6	4	1	5	2	3

We shall prove that this is generally true. Let the group G consist of the elements $A_1, \cdots, A_m$. We write down the multiplication table of the group:

$$\begin{array}{cccc} A_1 & A_2 & \cdots & A_m \\ A_2 & A_2A_2 & \cdots & A_2A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m & A_mA_2 & \cdots & A_mA_m \end{array}$$

Suppose this is not a Latin square. Then an element will occur twice in at least one row or at least one column, that is, we should have either

$$A_jA_i = A_jA_k, \qquad \text{for } i \neq k$$

or

$$A_jA_i = A_kA_i, \qquad \text{for } j \neq k.$$

Multiplying the first equation by A_j^{-1} on the left, we obtain $A_i = A_k$. Hence $i = k$. Similarly in the second case $j = k$, contrary to our assumption.

Two groups G and $\bar{G}$ are called isomorphic if we can map G into $\bar{G}$ in such a way that the mapping is not disturbed by multiplication. That is, if A is mapped on $\bar{A}$ and B on $\bar{B}$ and if $AB = C$ and $\bar{A}\bar{B} = \bar{C}$, then C must be mapped on $\bar{C}$. Such a mapping is called an isomorphism. If $G = \bar{G}$ then the mapping is called an automorphism. For instance, if we consider the remainder system mod m with addition as composition and j is any remainder, then the mapping $\bar{a} = ja$ is an automorphism. For if

$$a + b \equiv c(m)$$

then

$$aj + bj \equiv cj(m)$$

Some automorphisms establish a 1-to-1 correspondence between the elements of G. For instance, in the above example if j is prime to m the correspondence is bi-unique (that is only one element is mapped on any element of G) because if

$$aj \equiv bj(m),$$

and j is prime to m then

$$a \equiv b(m).$$

If j is not prime to m, the mapping would not be unique although it would still be an automorphism. From now on we shall consider only automorphisms which establish a 1-to-1 correspondence between the elements of G.

Let S be such an automorphism and denote by A^S the element into which A is mapped under the automorphism S. We put $(A^S)^S = A^{S^2}$, $(A^{S^2})^S = A^{S^3}$, etc. We also put $A^{S^0} = A$. We shall prove the following theorem:

Let S be an automorphism such that $S, S^2, \cdots, S^q$ map no element into itself except the element 1. *Then the Latin squares*

$$L_i = \begin{matrix} 1 & A_2 & \cdots & A_m \\ A_2^{S^i} & A_2^{S^i}A_2 & \cdots & A_2^{S^i}A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m^{S^i} & A_m^{S^i}A_2 & \cdots & A_m^{S^i}A_m \end{matrix} \qquad (i = 0, 1, \cdots, q)$$

are orthogonal.

Proof: Assume that L_i is not orthogonal to L_j. Let L_{ij} be the resulting square if L_j is superimposed on L_i. Then for some k and l and some r and s we should have the same pair of elements in the kth row and lth column and in the rth row and sth column. That is, we should have

$$A_k^{S^i}A_l = A_r^{S^i}A_s \tag{1}$$

$$A_k^{S^j}A_l = A_r^{S^j}A_s . \tag{2}$$

By taking the inverse elements it follows from (2) that

$$A_l^{-1}A_k^{-S^j} = A_s^{-1}A_r^{-S^j} . \tag{3}$$

Multiplying (1) and (3) we obtain

$$A_k^{S^i}A_k^{-S^j} = A_r^{S^i}A_r^{-S^j}.$$

Multiplying by $A_r^{-S^i}$ to the left, and by $A_k^{S^j}$ to the right, we obtain

$$A_r^{-S^i}A_k^{S^i} = A_r^{-S^j}A_k^{S^j}.$$

Since S^i and S^j are automorphisms we have

$$(A_r^{-1}A_k)^{S^i} = (A_r^{-1}A_k)^{S^j}.$$

Assuming $i > j$, then

$$[(A_r^{-1}A_k)^{S^j}]^{S^{i-j}} = (A_r^{-1}A_k)^{S^j}.$$

Because of $i \leq q, j \leq q$ we have $i \dot{-} j \leq q$. By assumption therefore S^{i-j} can can leave only 1 fixed. Therefore

$$(A_r^{-1}A_k)^{S^j} = 1.$$

Hence

$$A_r^{-1}A_k = 1$$

$$A_r = A_k .$$

But then also

$$A_l = A_s .$$

Therefore $r = k$ and $l = s$. Hence the two compartments of L_{ij} cannot be different and our statement is proved.

We see therefore that we can construct a set of $q + 1$ orthogonal Latin squares if we can find a group G and an automorphism S of G such that

$$S, S^2, \cdots, S^q$$

maps no element into itself except the unit element. If $q = m - 2$ and we write

$$L_i = \begin{matrix} 1 & A_2 & A_2^s & \cdots & A_2^{s^q} \\ A_2^{s^i} & A_2^{s^i}A_2 & \cdot & \cdots & A_2^{s^i}A_2^{s^q} \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ A_2^{s^{q+i}} & \cdot & \cdot & \cdots & A_2^{s^{q+i}}A_2^{s^q} \end{matrix}$$

then the $(k-1)$st row of L_{i+1} equals the k-th row of L_i and all squares may be obtained from L_0 by a cyclical permutation of the rows.

We shall now consider commutative groups of prime power order p^n defined by the relations

$$P_1^p = P_2^p = \cdots = P_n^p = 1, \qquad P_iP_j = P_jP_i .$$

The elements of this group G have the form

$$P_1^{e_1} \cdots P_n^{e_n} \qquad\qquad e_1, \cdots, e_n = 0, 1, \cdots, p-1.$$

We call $P_1 \cdots P_n$ a basis of G. We can easily change the basis. For instance if $P_1, \cdots, P_n$ is a basis then also $P_1, P_1P_2, \cdots, P_1P_n$ is a basis. For every expression we have

$$P_1^{e_1} \cdots P_n^{e_n} = P_1^{e_1-e_2-\cdots-e_n}(P_1P_2)^{e_2} \cdots (P_1P_n)^{e_n},$$

since G is commutative. Such a change in the basis defines an automorphism of G at the same time. For let $P_1', \cdots, P_n'$ be the new basis. We can map

$$P_1^{e_1} \cdots P_n^{e_n}$$

into

$$P_1'^{e_1} \cdots P_n'^{e_n} .$$

On the other hand an automorphism is determined if we know on what elements the basis elements are mapped.

It can be shown that every such group admits an automorphism S such that $S, S^2, \cdots, S^{p^n-2}$ leaves no element fixed except 1. Hence we can always construct a set of $p^n - 1$ orthogonal squares of side p^n if p is a prime. We shall give these automorphisms explicitly for the groups of order 8, 9, 16, 25 and 27.

As an example let us construct 7 orthogonal 8 sided squares. We shall use

the group G generated by P, Q, R where $P^2 = Q^2 = R^2 = 1$. We use the automorphism S where

$$P^S = Q \qquad Q^S = R \qquad R^S = PQ.$$

We then have $P^S = Q$, $P^{S^2} = R$, $P^{S^3} = PQ$, $P^{S^4} = P^SQ^S = QR$, $P^{S^5} = Q^SR^S = PQR$, $P^{S^6} = P^SQ^SR^S = QRPQ = PR$, $P^{S^7} = P^SR^S = QPQ = P$. If we write the elements in the order $1, P, P^S, P^{S^2}, \cdots, P^{S^6}$ we obtain the following multiplication table:

1	P	Q	R	PQ	QR	PQR	PR
P	1	PQ	PR	Q	PQR	QR	R
Q	PQ	1	QR	P	R	PR	PQR
R	PR	QR	1	PQR	Q	PQ	P
PQ	Q	P	PQR	1	PR	R	QR
QR	PQR	R	Q	PR	1	P	PQ
PQR	QR	PR	PQ	R	P	1	Q
PR	R	PQR	P	QR	PQ	Q	1

The other squares are then obtained by a cyclical permutation of the rows of this square. We now write 2 instead of P, 3 instead of Q, etc. and obtain:

$$L_0 = \begin{array}{cccccccc} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\ 2 & 1 & 5 & 8 & 3 & 7 & 6 & 4 \\ 3 & 5 & 1 & 6 & 2 & 4 & 8 & 7 \\ 4 & 8 & 6 & 1 & 7 & 3 & 5 & 2 \\ 5 & 3 & 2 & 7 & 1 & 8 & 4 & 6 \\ 6 & 7 & 4 & 3 & 8 & 1 & 2 & 5 \\ 7 & 6 & 8 & 5 & 4 & 2 & 1 & 3 \\ 8 & 4 & 7 & 2 & 6 & 5 & 3 & 1 \end{array} \qquad L_1 = \begin{array}{cccccccc} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\ 3 & 5 & 1 & 6 & 2 & 4 & 8 & 7 \\ 4 & 8 & 6 & 1 & 7 & 3 & 5 & 2 \\ 5 & 3 & 2 & 7 & 1 & 8 & 4 & 6 \\ 6 & 7 & 4 & 3 & 8 & 1 & 2 & 5 \\ 7 & 6 & 8 & 5 & 4 & 2 & 1 & 3 \\ 8 & 4 & 7 & 2 & 6 & 5 & 3 & 1 \\ 2 & 1 & 5 & 8 & 3 & 7 & 6 & 4 \end{array}$$

and so forth.

For the group of order 9, generated by P, Q with the relations $P^3 = Q^3 = 1$ the automorphism $P^S = Q, Q^S = PQ$ has the property that $S, S^2, \cdots, S^7$ maps no element into itself. For the group of order 16 we have 4 basis elements P, Q, R, T with $P^2 = Q^2 = R^2 = T^2 = 1$ and S can be given by $P^S = Q, Q^S = R, R^S = T, T^S = PT$.

For the group of order 25 we have two basis elements P, Q with $P^5 = Q^5 = 1$ and the automorphism is given by $P^S = Q, Q^S = P^3Q$.

The group of order 27 is generated by P, Q, R and the defining relations are $P^3 = Q^3 = R^3 = 1$. The automorphism is given by $P^S = Q, Q^S = R, R^S = P^2Q$.

We have now shown

THEOREM 3: *Let $m = p^n$ and let G be the commutative group generated by $P_1, \cdots, P_n$ which satisfy the relations $P_1^p = P_2^p = \cdots = P_n^p = 1$. Let S be an*

automorphism such that $P^{s^i} \neq P$ *if* $0 < i \leq m-2$, $P \neq 1$. *Then the Latin squares*

$$L_i = \begin{matrix} 1 & P & P^s & \cdots & P^{s^{m-2}} \\ P^{s^i} & P^{s^i}P & \cdots & \cdots & P^{s^i}P^{s^{m-2}} \\ P^{s^{1+i}} & P^{s^{1+i}}P & \cdots & \cdots & P^{s^{1+i}}P^{s^{m-2}} \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ P^{s^{m-2+i}} & P^{s^{m-2+i}}P & \cdots & \cdots & P^{s^{m-2+i}}P^{s^{m-2}} \end{matrix} \qquad (i = 0, 1, \cdots, m-2),$$

are orthogonal. L_i *is obtained from* L_{i-1} *by a cyclical permutation of its last* $m-1$ *rows.*

4. Remarks on the largest number of m-sided orthogonal Latin squares, for arbitrary m.

The general problem can be formulated as follows: Given a number m, what is the greatest number of orthogonal m-sided squares.

It is clear that this number cannot be larger than $m-1$. For we can by renaming the numbers of the squares always transform them without changing their orthogonality in such a way that the first row is $1, 2, \cdots m$. Hence the pairs $1\ 1, 2\ 2, \cdots, m\ m$, occur for any two squares in the first row of the resulting square. Hence the numbers in the first column and second row of the squares must be different from 1 and different from each other. But we have only the numbers $2, \cdots, m$ at our disposal and these are only $m-1$ numbers.

We have shown that if m is the power of a prime $m-1$ orthogonal squares can always be constructed by the use of groups. Hence our problem is solved if m is the power of a prime. Very little is known about numbers which are not prime powers. Tarry (*Compte Rendu*, 1900) has shown that no 6 sided Graeco-Latin square exists. It is conjectured but not yet proved that no Graeco-Latin square of side $4n+2$ exists. We shall, however, show the following: If $m = p_1^{e_1} \cdots p_n^{e_n}$ where p_i is a prime number ($p_i \neq p_j$ for $i \neq j$) and if $r =$ minimum $p_i^{e_i} - 1$ then r orthogonal Latin squares can be constructed from commutative groups of order m.

We take the group G of order m generated by e_1 elements of order p_1, e_2 elements of order p_2, $\cdots$, e_n elements of order p_n. We determine the automorphisms T_i of the subgroup generated by the elements of order p_i such that T_i, $T_i^2, \cdots, T_i^{p_i^{e_i}-2}$ leave no element of order p_i fixed. We define then an automorphism $\overline{T}_i$ of G generated by changing the basis elements of order p_i in the same way as they are changed by T_i and leaving the other basis elements fixed. Then

$$T = \overline{T}_1\overline{T}_2 \cdots \overline{T}_n$$

is an automorphism whose first $r-1$ powers leave no element fixed. Hence the r Latin squares

$$L_i = \begin{matrix} 1 & A_2 & \cdots & A_m \\ A_2^{T^i} & A_2^{T^i}A_2 & \cdots & A_2^{T^i}A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m^{T^i} & A_m^{T^i}A_2 & \cdots & A_m^{T^i}A_m \end{matrix} \qquad (i = 0, 1, \cdots, r-1)$$

are orthogonal.

TABLE I

1	P	Q	PQ	PR	QR²	PQR⁴	PR³	QR	PQR²	PR⁴	QR³	PQR	PR²	QR⁴	PQR³	R	R²	R⁴	R³
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2	1	4	3	17	10	15	20	13	6	19	16	9	18	7	12	5	14	11	8
3	4	1	2	13	18	11	16	17	14	7	20	5	10	19	8	9	6	15	12
4	3	2	1	9	14	19	12	5	18	15	8	17	6	11	20	13	10	7	16
5	17	13	9	18	16	3	19	10	12	1	7	6	20	4	15	14	8	2	11
6	10	18	14	16	19	5	4	20	11	13	1	8	7	17	2	12	15	9	3
7	15	11	19	3	5	20	6	2	17	12	14	1	9	8	18	4	13	16	10
8	20	16	12	19	4	6	17	7	3	18	13	15	1	10	9	11	2	14	5
9	13	17	5	10	20	2	7	18	8	4	19	14	16	1	11	6	12	3	15
10	6	14	18	12	11	17	3	8	19	9	2	20	15	5	1	16	7	13	4
11	19	7	15	1	13	12	18	4	9	20	10	3	17	16	6	2	5	8	14
12	16	20	8	7	1	14	13	19	2	10	17	11	4	18	5	15	3	6	9
13	9	5	17	6	8	1	15	14	20	3	11	18	12	2	19	10	16	4	7
14	18	10	6	20	7	9	1	16	15	17	4	12	19	13	3	8	11	5	2
15	7	19	11	4	17	8	10	1	5	16	18	2	13	20	14	3	9	12	6
16	12	8	20	15	2	18	9	11	1	6	5	19	3	14	17	7	4	10	13
17	5	9	13	14	12	4	11	6	16	2	15	10	8	3	7	18	20	1	19
18	14	6	10	8	15	13	2	12	7	5	3	16	11	9	4	20	19	17	1
19	11	15	7	2	9	16	14	3	13	8	6	4	5	12	10	1	17	20	18
20	8	12	16	11	3	10	5	15	4	14	9	7	2	6	13	19	1	18	17

We shall exemplify this by constructing 3 orthogonal squares of side 20. We use the group G generated by P, Q, R with the defining relations: $P^2 = Q^2 = 1$; $R^5 = 1$. The automorphisms are given by: $P^{\bar{T}_1} = Q$, $Q^{\bar{T}_1} = PQ$, $R^{\bar{T}_1} = R$, $P^{\bar{T}_2} = P$, $Q^{\bar{T}_2} = Q$, $R^{\bar{T}_2} = R$. Hence $T = \bar{T}_1\bar{T}_2$ is given by: $P^T = Q$, $Q^T = TQ$, $R^T = R^2$. Therefore we have: $P^T = Q$, $P^{T^2} = PQ$, $P^{T^3} = P^TQ^T = P$, $(PR)^T = QR^2$, $(PR)^{T^2} = PQR^4$, $(PR)^{T^3} = PR^3$, $(PR)^{T^4} = QR$, $(PR)^{T^5} = PQR^2$, $(PR)^{T^6} = PR^4$, $(PR)^{T^7} = QR^3$, $(PR)^{T^8} = PQR$, $(PR)^{T^9} = PR^2$, $(PR)^{T^{10}} = QR^4$, $(PR)^{T^{11}} = PQR^3$, $(PR)^{T^{12}} = PR$, $R^T = R^2$, $R^{T^2} = R^4$, $R^{T^3} = R^3$, $R^{T^4} = R$.

We need only construct one key square if we write down the elements in the way in which they are written above. Then we have only to mark the end of each cycle. Thus in our present case we have:

$1 \mid P, Q, PQ \mid PR, QR^2, PQR^4, PR^3, QR, PQR^2, PR^4, QR^3, PQR, PR^2, QR^4,$
$PQR^3 \mid R, R^2, R^4, R^3 \mid$

The vertical lines mark the cycles in which the elements are permuted by the automorphisms. We then write down the key square in Table I. From this key square we can easily obtain a set of 3 orthogonal squares by permuting the

TABLE II

1,1	2,2	3,3	4,4	5,5	6,6	7,7	8,8	9,9	10,10
1	2	3	4	5	6	7	8	9	10
2,3	1,4	4,1	3,2	17,13	10,18	15,11	20,16	13,17	6,14
4	3	2	1	9	14	19	12	5	18
3,4	4,3	1,2	2,1	13,9	18,14	11,19	16,12	17,5	14,18
2	1	4	3	17	10	15	20	13	6
4,2	3,1	2,4	1,3	9,17	14,10	19,15	12,20	5,13	18,6
3	4	1	2	13	18	11	16	17	14
5,6	17,10	13,18	9,14	18,16	16,19	3,5	19,4	10,20	12,11
7	15	11	19	3	5	20	6	2	17
6,7	10,15	18,11	14,19	16,3	19,5	5,20	4,6	20,2	11,17
8	20	16	12	19	4	6	17	7	3
7,8	15,20	11,16	19,12	3,19	5,4	20,6	6,17	2,7	17,3
9	13	17	5	10	20	2	7	18	8
8,9	20,13	16,17	12,5	19,10	4,20	6,2	17,7	7,18	3,8
10	6	14	18	12	11	17	3	8	19
9,10	13,6	7,14	5,18	10,12	20,11	2,17	7,3	18,8	8,19
11	19	7	15	1	13	12	18	4	9
10,11	6,19	14,7	18,15	12,1	11,13	17,12	3,18	8,4	19,9
12	16	20	8	7	1	14	13	19	2
11,12	19,16	7,20	15,8	1,7	13,1	12,14	18,13	4,19	9,2
13	9	5	17	6	8	1	15	14	20
12,13	16,9	20,5	8,17	7,6	1,8	14,1	13,15	19,14	2,20
14	18	10	6	20	7	9	1	16	15
13,14	9,18	5,10	17,6	6,20	8,7	1,9	15,1	14,16	20,15
15	7	19	11	4	17	8	10	1	5
14,15	18,7	10,19	6,11	20,4	7,17	9,8	1,10	16,1	15,5
16	12	8	20	15	2	18	9	11	1
15,16	7,12	19,8	11,20	4,15	17,2	8,18	10,9	1,11	5,1
5	17	13	9	18	16	3	19	10	12
16,5	12,17	8,13	20,9	15,18	2,16	18,3	9,19	11,10	1,12
6	10	18	14	16	19	5	4	20	11
17,18	5,14	9,6	13,10	14,8	12,15	4,13	11,2	6,12	16,7
19	11	15	7	2	9	16	14	3	13
18,19	14,11	6,15	10,7	8,2	15,9	13,16	2,14	12,3	7,13
20	8	12	16	11	3	10	5	15	4
19,20	11,8	15,12	7,16	2,11	9,3	16,10	14,5	3,15	13,4
17	5	9	13	14	12	4	11	6	16
20,17	8,5	12,9	16,13	11,14	3,12	10,4	5,11	15,6	4,16
18	14	6	10	8	15	13	2	12	7

rows within the cycles indicated. Because of space difficulties we give only the first half of the square in Table II.

One might hope that with other groups more than r = minimum $p_i^{e_i} - 1$ orthogonal squares might be obtained. It has been shown however that using any group and its automorphisms at most r orthogonal squares can be obtained.

A more general method based on groups is given in a recent paper (H. B. Mann, "The construction of sets of orthogonal Latin squares," *Annals of Math. Stat.*, Vol. 13 (1942)). It can be shown that also with this more general method no $4n + 2$ sided Graeco-Latin square can be constructed.

ADDITIONAL LITERATURE

R. C. Bose: "On the application of the properties of Galois-fields to the construction of completely orthogonalized Latin squares," *Sankhyā*, 1939.

"On completely orthogonalized sets of Latin squares," *Sankhyā*, 1941.

ON THE DEPENDENCE OF SAMPLING INSPECTION PLANS UPON POPULATION DISTRIBUTIONS

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1. Introduction. The foundations of the science of quality control and quality determination have been laid by W. A. Shewhart [1, 2]. His ideas pervade what follows, but they are too well known to require discussion here. There is, however, one that should be specifically mentioned, that of *statistically controlled production*, because it provides the justification for the basic assumption of this paper: *When production is statistically controlled, there exists a probability, $P(N, X)$, that a lot of size N will contain X defective items.* Shewhart has given a complete discussion of assumptions of this nature.

Sampling inspection of lots may take one of two courses:

(a) Item inspection, in which a lot is accepted or completely inspected on the basis of one or more samples drawn from the lot.

(b) Lot inspection, in which a lot is accepted or rejected on the basis of one or more samples drawn from the lot.

The former has been extensively studied by Dodge and Romig [3, 4, 5]; the latter has received little attention, but some of the basic ideas of Dodge and Romig are applicable to this case also.

In this paper the approach to the general problem of lot inspection will be different from that of Dodge and Romig in one important respect: The role of the population distribution function will be emphasized, whereas they have directed their attention to methods which require no knowledge of the population distribution. Their techniques are particularly valuable when a probability distribution does not exist, that is, when production is not statistically controlled. The interest here will be in the inspection of lots which may be regarded as having been drawn from a statistical population. After the first sample from the first lot has been drawn, something is known of the distribution of that population, and as the inspection proceeds a great body of knowledge may be accumulated. Here, if ever, is a real opportunity to explore and to use a population distribution. The very nature of inspection supplies a continuous flow of information about it. To neglect this information would be wasteful indeed.

It is, therefore, the object of this paper to point the way to more efficient inspection procedures for situations in which production is statistically controlled. The inspection procedure will be considered to be an inferential process—on the basis of one or more samples, and with whatever information is available about the parent distribution, an inference will be made regarding the quality

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is equal to a power of a mod p. For example, 3 is a primitive root mod 7, for $3^0 \equiv 1\ (7)$, $3^1 \equiv 3(7)$, $3^2 \equiv 2(7)$, $3^3 \equiv 6(7)$, $3^4 \equiv 4(7)$, $3^5 \equiv 5(7)$.

For any number a we must have $a^{p-1} \equiv 1\ (p)$. We will prove this equation for primitive roots only, since we do not need the general case. Let a be a primitive root and assume that

$$a^{p-1} \equiv b \equiv a^q\ (p), \qquad \text{with } q < p-1.$$

Then we would have

$$a^{p-1-q} \equiv a^{p'} \equiv 1\ (p), \qquad \text{with } p' < p-1.$$

Hence we can obtain at most $p-2$ different remainders $a^0 a^1, \cdots, a^{p'-1}$ and a would not be a primitive root.

We now form

$$\bar{L}_i = \begin{matrix} 0 & 1 & \cdots & p-1 \\ a^{0+i} & 1+a^{0+i} & \cdots & p-1+a^{0+i} \\ a^{1+i} & 1+a^{1+i} & \cdots & p-1+a^{1+i} \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ a^{p-2+i} & 1+a^{p-2+i} & \cdots & p-1+a^{p-2+i} \end{matrix} \quad (i = 0, 1, \cdots, p-2)$$

Exactly as in the case of the L_j of Theorem 1 it can be shown that $\bar{L}_i$ is orthogonal to $\bar{L}_j$ if $i \neq j$. For $k < p-1$ the k-th row of $\bar{L}_i$ equals the $(k-1)$st row of $\bar{L}_{i+1}$ and since $a^{p-1} \equiv 1\ (p)$ the last row of $\bar{L}_{i+1}$ equals the first row of $\bar{L}_i$. Hence $\bar{L}_{i+1}$ is obtained from $\bar{L}_i$ by a cyclical permutation of the $(p-1)$ last rows. It is then only necessary to construct the first square. The others can be obtained by a cyclic permutation of the $(p-1)$ last rows. We shall exemplify this by constructing a set of 6 seven-sided orthogonal squares.

L_1	L_2	L_3
0 1 2 3 4 5 6	0 1 2 3 4 5 6	0 1 2 3 4 5 6
1 2 3 4 5 6 0	3 4 5 6 0 1 2	2 3 4 5 6 0 1
3 4 5 6 0 1 2	2 3 4 5 6 0 1	6 0 1 2 3 4 5
2 3 4 5 6 0 1	6 0 1 2 3 4 5	4 5 6 0 1 2 3
6 0 1 2 3 4 5	4 5 6 0 1 2 3	5 6 0 1 2 3 4
4 5 6 0 1 2 3	5 6 0 1 2 3 4	1 2 3 4 5 6 0
5 6 0 1 2 3 4	1 2 3 4 5 6 0	3 4 5 6 0 1 2

L_4	L_5	L_6
0 1 2 3 4 5 6	0 1 2 3 4 5 6	0 1 2 3 4 5 6
6 0 1 2 3 4 5	4 5 6 0 1 2 3	5 6 0 1 2 3 4
4 5 6 0 1 2 3	5 6 0 1 2 3 4	1 2 3 4 5 6 0
5 6 0 1 2 3 4	1 2 3 4 5 6 0	3 4 5 6 0 1 2
1 2 3 4 5 6 0	3 4 5 6 0 1 2	2 3 4 5 6 0 1
3 4 5 6 0 1 2	2 3 4 5 6 0 1	6 0 1 2 3 4 5
2 3 4 5 6 0 1	6 0 1 2 3 4 5	4 5 6 0 1 2 3

In the theory of numbers it is shown that a primitive root exists for every prime number. If p is not too large a primitive root can easily be found by trial and error. We give a list of primitive roots for all primes under 30:

Prime number	Primitive root
3	2
5	2
7	3
11	2
13	2
17	3
19	2
23	5
29	2

In computing the first row of the first square it is not necessary to actually compute all powers of the primitive root. We can take advantage of the fact that a congruence may be multiplied by a number. Thus, for instance, for the first row of the 11-sided square we have $2^0 \equiv 1\ (11)$ $2^1 \equiv 2\ (11)$ $2^2 \equiv 4\ (11)$ $2^3 \equiv 8\ (11)$ $2^4 \equiv 5\ (11)$ $2^5 \equiv 2.5 \equiv 10\ (11)$ but $10 \equiv -1\ (11)$, hence we have without further computation $2^6 \equiv -2 \equiv 9\ (11)$ $2^7 \equiv -4 \equiv 7\ (11)$ $2^8 \equiv -8 \equiv 3\ (11)$ $2^9 \equiv -5 \equiv 6\ (11)$.

3. Complete sets of m-sided orthogonal Latin squares, where m is the power of a prime.

We have seen that we can always construct $m - 1$ orthogonal Latin squares if m is a prime number. We shall show how to construct $m - 1$ orthogonal Latin squares if m is the power of a prime. However, if we need only a Graeco-Latin square of side m and if m is odd, then we can use the following theorem:

THEOREM 2: *If m is odd, then the squares*

$$L_1 = \begin{array}{cccc} 0 & 1 & \cdots & m-1 \\ 1 & 1+1 & \cdots & m-1+1 \\ 2 & 1+2 & \cdots & m-1+2 \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ m-1 & 1+m-1 & \cdots & m-1+m-1 \end{array}$$

$$L_2 = \begin{array}{cccc} 0 & 1 & \cdots & m-1 \\ 2 & 1+2 & \cdots & m-1+2 \\ 2.2 & 1+2.2 & \cdots & m-1+2.2 \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ 2(m-1) & 1+2(m-1) & \cdots & m-1+2(m-1) \end{array}$$

are orthogonal.

The proof is similar to the proof of Theorem 1. We have to use the fact that 2 is prime to m.

We shall now prove the following statement: *For every remainder* $a \not\equiv 0(p)$ *there exists another remainder* a^{-1} *such that* $a \cdot a^{-1} \equiv 1(p)$.

PROOF: We form the sequence $a, a^2, \cdots, a^n, \cdots$. Since there is only a finite number of remainders, there must exist 2 values i and j such that

$$a^i \equiv a^j(p)$$

Let $i > j$. Then since a is prime to p we may divide by a^j. Putting $i - j = d$, we obtain

$$a^{i-j} = a^d \equiv 1(p).$$

Hence we may take $a^{-1} = a^{d-1}$ and our statement is proved. Thus we see that the system of remainders mod p with respect to addition as well as with respect to multiplication if 0 is excluded satisfies the following postulates:

(1) For every pair of elements A, B there is defined a product $A \cdot B$ within the system such that for any 3 elements A, B and C

$$A \cdot (B \cdot C) = (A \cdot B) \cdot C \qquad \text{(associative law)}$$

The "multiplication" may be any sort of composition. For example, either addition or multiplication of remainder classes.

(2) There exists a unit element 1 such that

$$A \cdot 1 = 1 \cdot A = A.$$

(3) For every A in the system there exists an element A^{-1} such that

$$A \cdot A^{-1} = A^{-1} \cdot A = 1.$$

The unit element will be 0 if we consider the remainder classes with addition as composition. It will be 1 if multiplication is the composition. The inverse of a is $-a$ for the additive system, a^{-1} for the multiplicative system.

A system satisfying (1), (2) and (3) is called a group. The property $A \cdot B = B \cdot A$ is usually not postulated. If a group fulfills this condition, then it is called a commutative group or an Abelian group. A group can be defined by its generating elements. For example, let G be generated by the elements P, Q with the relations $P^2 = 1$, $Q^3 = 1$ and $PQ = Q^2P$. We then obtain the elements of G as $1, P, Q, PQ, PQ^2, Q^2$. The rules for the multiplication can be written down in the form of a table:

1	P	Q	PQ	PQ^2	Q^2
P	1	PQ	Q	Q^2	PQ^2
Q	PQ^2	Q^2	P	PQ	1
PQ	Q^2	PQ^2	1	Q	P
PQ^2	Q	P	Q^2	1	PQ
Q^2	PQ	1	PQ^2	P	Q

By inspection one can see that taking the elements of our group as symbols the multiplication table forms a Latin square. For instance, if we identify P with 2, Q with 3, etc. we obtain from the table above

1	2	3	4	5	6
2	1	4	3	6	5
3	5	6	2	4	1
4	6	5	1	3	2
5	3	2	6	1	4
6	4	1	5	2	3

We shall prove that this is generally true. Let the group G consist of the elements $A_1, \cdots, A_m$. We write down the multiplication table of the group:

$$\begin{array}{cccc} A_1 & A_2 & \cdots & A_m \\ A_2 & A_2A_2 & \cdots & A_2A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m & A_mA_2 & \cdots & A_mA_m \end{array}$$

Suppose this is not a Latin square. Then an element will occur twice in at least one row or at least one column, that is, we should have either

$$A_jA_i = A_jA_k, \qquad \text{for } i \neq k$$

or

$$A_jA_i = A_kA_i, \qquad \text{for } j \neq k.$$

Multiplying the first equation by A_j^{-1} on the left, we obtain $A_i = A_k$. Hence $i = k$. Similarly in the second case $j = k$, contrary to our assumption.

Two groups G and $\bar{G}$ are called isomorphic if we can map G into $\bar{G}$ in such a way that the mapping is not disturbed by multiplication. That is, if A is mapped on $\bar{A}$ and B on $\bar{B}$ and if $AB = C$ and $\bar{A}\bar{B} = \bar{C}$, then C must be mapped on $\bar{C}$. Such a mapping is called an isomorphism. If $G = \bar{G}$ then the mapping is called an automorphism. For instance, if we consider the remainder system mod m with addition as composition and j is any remainder, then the mapping $\bar{a} = ja$ is an automorphism. For if

$$a + b \equiv c(m)$$

then

$$aj + bj \equiv cj(m)$$

Some automorphisms establish a 1-to-1 correspondence between the elements of G. For instance, in the above example if j is prime to m the correspondence is bi-unique (that is only one element is mapped on any element of G) because if

$$aj \equiv bj(m),$$

and j is prime to m then

$$a \equiv b(m).$$

If j is not prime to m, the mapping would not be unique although it would still be an automorphism. From now on we shall consider only automorphisms which establish a 1-to-1 correspondence between the elements of G.

Let S be such an automorphism and denote by A^S the element into which A is mapped under the automorphism S. We put $(A^S)^S = A^{S^2}$, $(A^{S^2})^S = A^{S^3}$, etc. We also put $A^{S^0} = A$. We shall prove the following theorem:

Let S be an automorphism such that S, S^2, $\cdots$, S^q map no element into itself except the element 1. *Then the Latin squares*

$$L_i = \begin{matrix} 1 & A_2 & \cdots & A_m \\ A_2^{S^i} & A_2^{S^i}A_2 & \cdots & A_2^{S^i}A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m^{S^i} & A_m^{S^i}A_2 & \cdots & A_m^{S^i}A_m \end{matrix} \qquad (i = 0, 1, \cdots, q)$$

are orthogonal.

Proof: Assume that L_i is not orthogonal to L_j. Let L_{ij} be the resulting square if L_j is superimposed on L_i. Then for some k and l and some r and s we should have the same pair of elements in the kth row and lth column and in the rth row and sth column. That is, we should have

$$A_k^{S^i}A_l = A_r^{S^i}A_s \tag{1}$$

$$A_k^{S^j}A_l = A_r^{S^j}A_s . \tag{2}$$

By taking the inverse elements it follows from (2) that

$$A_l^{-1}A_k^{-S^j} = A_s^{-1}A_r^{-S^j} . \tag{3}$$

Multiplying (1) and (3) we obtain

$$A_k^{S^i}A_k^{-S^j} = A_r^{S^i}A_r^{-S^j}.$$

Multiplying by $A_r^{-S^i}$ to the left, and by $A_k^{S^j}$ to the right, we obtain

$$A_r^{-S^i}A_k^{S^i} = A_r^{-S^j}A_k^{S^j}.$$

Since S^i and S^j are automorphisms we have

$$(A_r^{-1}A_k)^{S^i} = (A_r^{-1}A_k)^{S^j}.$$

Assuming $i > j$, then

$$[(A_r^{-1}A_k)^{S^j}]^{S^{i-j}} = (A_r^{-1}A_k)^{S^j}.$$

Because of $i \leq q, j \leq q$ we have $i - j \leq q$. By assumption therefore S^{i-j} can can leave only 1 fixed. Therefore

$$(A_r^{-1}A_k)^{S^j} = 1.$$

Hence

$$A_r^{-1}A_k = 1$$

$$A_r = A_k .$$

But then also

$$A_l = A_s .$$

Therefore $r = k$ and $l = s$. Hence the two compartments of L_{ij} cannot be different and our statement is proved.

We see therefore that we can construct a set of $q + 1$ orthogonal Latin squares if we can find a group G and an automorphism S of G such that

$$S, S^2, \cdots, S^q$$

maps no element into itself except the unit element. If $q = m - 2$ and we write

$$L_i = \begin{matrix} 1 & A_2 & A_2^S & \cdots & A_2^{S^q} \\ A_2^{S^i} & A_2^{S^i}A_2 & \cdot & \cdots & A_2^{S^i}A_2^{S^q} \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ A_2^{S^{q+i}} & \cdot & \cdot & \cdots & A_2^{S^{q+i}}A_2^{S^q} \end{matrix}$$

then the $(k-1)$st row of L_{i+1} equals the k-th row of L_i and all squares may be obtained from L_0 by a cyclical permutation of the rows.

We shall now consider commutative groups of prime power order p^n defined by the relations

$$P_1^p = P_2^p = \cdots = P_n^p = 1, \qquad P_iP_j = P_jP_i .$$

The elements of this group G have the form

$$P_1^{e_1} \cdots P_n^{e_n} \qquad\qquad e_1, \cdots, e_n = 0, 1, \cdots, p-1.$$

We call $P_1 \cdots P_n$ a basis of G. We can easily change the basis. For instance if $P_1, \cdots, P_n$ is a basis then also $P_1, P_1P_2, \cdots, P_1P_n$ is a basis. For every expression we have

$$P_1^{e_1} \cdots P_n^{e_n} = P_1^{e_1-e_2-\cdots-e_n}(P_1P_2)^{e_2} \cdots (P_1P_n)^{e_n},$$

since G is commutative. Such a change in the basis defines an automorphism of G at the same time. For let $P_1', \cdots, P_n'$ be the new basis. We can map

$$P_1^{e_1} \cdots P_n^{e_n}$$

into

$$P_1'^{e_1} \cdots P_n'^{e_n} .$$

On the other hand an automorphism is determined if we know on what elements the basis elements are mapped.

It can be shown that every such group admits an automorphism S such that $S, S^2, \cdots, S^{p^n-2}$ leaves no element fixed except 1. Hence we can always construct a set of $p^n - 1$ orthogonal squares of side p^n if p is a prime. We shall give these automorphisms explicitly for the groups of order 8, 9, 16, 25 and 27.

As an example let us construct 7 orthogonal 8 sided squares. We shall use

the group G generated by P, Q, R where $P^2 = Q^2 = R^2 = 1$. We use the automorphism S where

$$P^s = Q \qquad Q^s = R \qquad R^s = PQ.$$

We then have $P^s = Q$, $P^{s^2} = R$, $P^{s^3} = PQ$, $P^{s^4} = P^sQ^s = QR$, $P^{s^5} = Q^sR^s = PQR$, $P^{s^6} = P^sQ^sR^s = QRPQ = PR$, $P^{s^7} = P^sR^s = QPQ = P$. If we write the elements in the order $1, P, P^s, P^{s^2}, \cdots, P^{s^6}$ we obtain the following multiplication table:

1	P	Q	R	PQ	QR	PQR	PR
P	1	PQ	PR	Q	PQR	QR	R
Q	PQ	1	QR	P	R	PR	PQR
R	PR	QR	1	PQR	Q	PQ	P
PQ	Q	P	PQR	1	PR	R	QR
QR	PQR	R	Q	PR	1	P	PQ
PQR	QR	PR	PQ	R	P	1	Q
PR	R	PQR	P	QR	PQ	Q	1

The other squares are then obtained by a cyclical permutation of the rows of this square. We now write 2 instead of P, 3 instead of Q, etc. and obtain:

$$L_0 = \begin{array}{cccccccc} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\ 2 & 1 & 5 & 8 & 3 & 7 & 6 & 4 \\ 3 & 5 & 1 & 6 & 2 & 4 & 8 & 7 \\ 4 & 8 & 6 & 1 & 7 & 3 & 5 & 2 \\ 5 & 3 & 2 & 7 & 1 & 8 & 4 & 6 \\ 6 & 7 & 4 & 3 & 8 & 1 & 2 & 5 \\ 7 & 6 & 8 & 5 & 4 & 2 & 1 & 3 \\ 8 & 4 & 7 & 2 & 6 & 5 & 3 & 1 \end{array} \qquad L_1 = \begin{array}{cccccccc} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\ 3 & 5 & 1 & 6 & 2 & 4 & 8 & 7 \\ 4 & 8 & 6 & 1 & 7 & 3 & 5 & 2 \\ 5 & 3 & 2 & 7 & 1 & 8 & 4 & 6 \\ 6 & 7 & 4 & 3 & 8 & 1 & 2 & 5 \\ 7 & 6 & 8 & 5 & 4 & 2 & 1 & 3 \\ 8 & 4 & 7 & 2 & 6 & 5 & 3 & 1 \\ 2 & 1 & 5 & 8 & 3 & 7 & 6 & 4 \end{array}$$

and so forth.

For the group of order 9, generated by P, Q with the relations $P^3 = Q^3 = 1$ the automorphism $P^s = Q, Q^s = PQ$ has the property that $S, S^2, \cdots, S^7$ maps no element into itself. For the group of order 16 we have 4 basis elements P, Q, R, T with $P^2 = Q^2 = R^2 = T^2 = 1$ and S can be given by $P^s = Q, Q^s = R, R^s = T, T^s = PT$.

For the group of order 25 we have two basis elements P, Q with $P^5 = Q^5 = 1$ and the automorphism is given by $P^s = Q, Q^s = P^3Q$.

The group of order 27 is generated by P, Q, R and the defining relations are $P^3 = Q^3 = R^3 = 1$. The automorphism is given by $P^s = Q, Q^s = R, R^s = P^2Q$.

We have now shown

THEOREM 3: *Let $m = p^n$ and let G be the commutative group generated by $P_1, \cdots, P_n$ which satisfy the relations $P_1^p = P_2^p = \cdots = P_n^p = 1$. Let S be an*

automorphism such that $P^{s^i} \neq P$ if $0 < i \leq m-2$, $P \neq 1$. *Then the Latin squares*

$$L_i = \begin{matrix} 1 & P & P^2 & \cdots & P^{s^{m-2}} \\ P^{s^i} & P^{s^i}P & \cdots & \cdots & P^{s^i}P^{s^{m-2}} \\ P^{s^{1+i}} & P^{s^{1+i}}P & \cdots & \cdots & P^{s^{1+i}}P^{s^{m-2}} \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdots & \cdot \\ P^{s^{m-2+i}} & P^{s^{m-2+i}}P & \cdots & \cdots & P^{s^{m-2+i}}P^{s^{m-2}} \end{matrix} \qquad (i = 0, 1, \cdots, m-2),$$

are orthogonal. L_i *is obtained from* L_{i-1} *by a cyclical permutation of its last* $m-1$ *rows.*

4. Remarks on the largest number of m-sided orthogonal Latin squares, for arbitrary m.

The general problem can be formulated as follows: Given a number m, what is the greatest number of orthogonal m-sided squares.

It is clear that this number cannot be larger than $m-1$. For we can by renaming the numbers of the squares always transform them without changing their orthogonality in such a way that the first row is $1, 2, \cdots m$. Hence the pairs $1\ 1, 2\ 2, \cdots, m\ m$, occur for any two squares in the first row of the resulting square. Hence the numbers in the first column and second row of the squares must be different from 1 and different from each other. But we have only the numbers $2, \cdots, m$ at our disposal and these are only $m-1$ numbers.

We have shown that if m is the power of a prime $m-1$ orthogonal squares can always be constructed by the use of groups. Hence our problem is solved if m is the power of a prime. Very little is known about numbers which are not prime powers. Tarry (*Compte Rendu*, 1900) has shown that no 6 sided Graeco-Latin square exists. It is conjectured but not yet proved that no Graeco-Latin square of side $4n+2$ exists. We shall, however, show the following: If $m = p_1^{e_1} \cdots p_n^{e_n}$ where p_i is a prime number ($p_i \neq p_j$ for $i \neq j$) and if $r =$ minimum $p_i^{e_i} - 1$ then r orthogonal Latin squares can be constructed from commutative groups of order m.

We take the group G of order m generated by e_1 elements of order p_1, e_2 elements of order p_2, $\cdots$, e_n elements of order p_n. We determine the automorphisms T_i of the subgroup generated by the elements of order p_i such that T_i, T_i^2, $\cdots$, $T_i^{p_i^{e_i}-2}$ leave no element of order p_i fixed. We define then an automorphism $\overline{T}_i$ of G generated by changing the basis elements of order p_i in the same way as they are changed by T_i and leaving the other basis elements fixed. Then

$$T = \overline{T}_1\overline{T}_2 \cdots \overline{T}_n$$

is an automorphism whose first $r-1$ powers leave no element fixed. Hence the r Latin squares

$$L_i = \begin{matrix} 1 & A_2 & \cdots & A_m \\ A_2^{T^i} & A_2^{T^i}A_2 & \cdots & A_2^{T^i}A_m \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ A_m^{T^i} & A_m^{T^i}A_2 & \cdots & A_m^{T^i}A_m \end{matrix} \qquad (i = 0, 1, \cdots, r-1)$$

are orthogonal.

TABLE I

1	P	Q	PQ	PR	QR²	PQR⁴	PR³	QR	PQR³	PR⁴	QR³	PQR	PR²	QR⁴	PQR²	R	R²	R⁴	R³
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2	1	4	3	17	10	15	20	13	6	19	16	9	18	7	12	5	14	11	8
3	4	1	2	13	18	11	16	17	14	7	20	5	10	19	8	9	6	15	12
4	3	2	1	9	14	19	12	5	18	15	8	17	6	11	20	13	10	7	16
5	17	13	9	18	16	3	19	10	12	1	7	6	20	4	15	14	8	2	11
6	10	18	14	16	19	5	4	20	11	13	1	8	7	17	2	12	15	9	3
7	15	11	19	3	5	20	6	2	17	12	14	1	9	8	18	4	13	16	10
8	20	16	12	19	4	6	17	7	3	18	13	15	1	10	9	11	2	14	5
9	13	17	5	10	20	2	7	18	8	4	19	14	16	1	11	6	12	3	15
10	6	14	18	12	11	17	3	8	19	9	2	20	15	5	1	16	7	13	4
11	19	7	15	1	13	12	18	4	9	20	10	3	17	16	6	2	5	8	14
12	16	20	8	7	1	14	13	19	2	10	17	11	4	18	5	15	3	6	9
13	9	5	17	6	8	1	15	14	20	3	11	18	12	2	19	10	16	4	7
14	18	10	6	20	7	9	1	16	15	17	4	12	19	13	3	8	11	5	2
15	7	19	11	4	17	8	10	1	5	16	18	2	13	20	14	3	9	12	6
16	12	8	20	15	2	18	9	11	1	6	5	19	3	14	17	7	4	10	13
17	5	9	13	14	12	4	11	6	16	2	15	10	8	3	7	18	20	1	19
18	14	6	10	8	15	13	2	12	7	5	3	16	11	9	4	20	19	17	1
19	11	15	7	2	9	16	14	3	13	8	6	4	5	12	10	1	17	20	18
20	8	12	16	11	3	10	5	15	4	14	9	7	2	6	13	19	1	18	17

We shall exemplify this by constructing 3 orthogonal squares of side 20. We use the group G generated by P, Q, R with the defining relations: $P^2 = Q^2 = 1$; $R^5 = 1$. The automorphisms are given by: $P^{\overline{T}_1} = Q$, $Q^{\overline{T}_1} = PQ$, $R^{\overline{T}_1} = R$, $P^{\overline{T}_2} = P$, $Q^{\overline{T}_2} = Q$, $R^{\overline{T}_2} = R$. Hence $T = \overline{T}_1\overline{T}_2$ is given by: $P^T = Q$, $Q^T = TQ$, $R^T = R^2$. Therefore we have: $P^T = Q$, $P^{T^2} = PQ$, $P^{T^3} = P^TQ^T = P$, $(PR)^T = QR^2$, $(PR)^{T^2} = PQR^4$, $(PR)^{T^3} = PR^3$, $(PR)^{T^4} = QR$, $(PR)^{T^5} = PQR^2$, $(PR)^{T^6} = PR^4$, $(PR)^{T^7} = QR^3$, $(PR)^{T^8} = PQR$, $(PR)^{T^9} = PR^2$, $(PR)^{T^{10}} = QR^4$, $(PR)^{T^{11}} = PQR^3$, $(PR)^{T^{12}} = PR$, $R^T = R^2$, $R^{T^2} = R^4$, $R^{T^3} = R^3$, $R^{T^4} = R$.

We need only construct one key square if we write down the elements in the way in which they are written above. Then we have only to mark the end of each cycle. Thus in our present case we have:

$1 \mid P, Q, PQ \mid PR, QR^2, PQR^4, PR^3, QR, PQR^2, PR^4, QR^3, PQR, PR^2, QR^4,$
$PQR^3 \mid R, R^2, R^4, R^3 \mid$

The vertical lines mark the cycles in which the elements are permuted by the automorphisms. We then write down the key square in Table I. From this key square we can easily obtain a set of 3 orthogonal squares by permuting the

TABLE II

1,1	2,2	3,3	4,4	5,5	6,6	7,7	8,8	9,9	10,10
1	2	3	4	5	6	7	8	9	10
2,3	1,4	4,1	3,2	17,13	10,18	15,11	20,16	13,17	6,14
4	3	2	1	9	14	19	12	5	18
3,4	4,3	1,2	2,1	13,9	18,14	11,19	16,12	17,5	14,18
2	1	4	3	17	10	15	20	13	6
4,2	3,1	2,4	1,3	9,17	14,10	19,15	12,20	5,13	18,6
3	4	1	2	13	18	11	16	17	14
5,6	17,10	13,18	9,14	18,16	16,19	3,5	19,4	10,20	12,11
7	15	11	19	3	5	20	6	2	17
6,7	10,15	18,11	14,19	16,3	19,5	5,20	4,6	20,2	11,17
8	20	16	12	19	4	6	17	7	3
7,8	15,20	11,16	19,12	3,19	5,4	20,6	6,17	2,7	17,3
9	13	17	5	10	20	2	7	18	8
8,9	20,13	16,17	12,5	19,10	4,20	6,2	17,7	7,18	3,8
10	6	14	18	12	11	17	3	8	19
9,10	13,6	7,14	5,18	10,12	20,11	2,17	7,3	18,8	8,19
11	19	7	15	1	13	12	18	4	9
10,11	6,19	14,7	18,15	12,1	11,13	17,12	3,18	8,4	19,9
12	16	20	8	7	1	14	13	19	2
11,12	19,16	7,20	15,8	1,7	13,1	12,14	18,13	4,19	9,2
13	9	5	17	6	8	1	15	14	20
12,13	16,9	20,5	8,17	7,6	1,8	14,1	13,15	19,14	2,20
14	18	10	6	20	7	9	1	16	15
13,14	9,18	5,10	17,6	6,20	8,7	1,9	15,1	14,16	20,15
15	7	19	11	4	17	8	10	1	5
14,15	18,7	10,19	6,11	20,4	7,17	9,8	1,10	16,1	15,5
16	12	8	20	15	2	18	9	11	1
15,16	7,12	19,8	11,20	4,15	17,2	8,18	10,9	1,11	5,1
5	17	13	9	18	16	3	19	10	12
16,5	12,17	8,13	20,9	15,18	2,16	18,3	9,19	11,10	1,12
6	10	18	14	16	19	5	4	20	11
17,18	5,14	9,6	13,10	14,8	12,15	4,13	11,2	6,12	16,7
19	11	15	7	2	9	16	14	3	13
18,19	14,11	6,15	10,7	8,2	15,9	13,16	2,14	12,3	7,13
20	8	12	16	11	3	10	5	15	4
19,20	11,8	15,12	7,16	2,11	9,3	16,10	14,5	3,15	13,4
17	5	9	13	14	12	4	11	6	16
20,17	8,5	12,9	16,13	11,14	3,12	10,4	5,11	15,6	4,16
18	14	6	10	8	15	13	2	12	7

rows within the cycles indicated. Because of space difficulties we give only the first half of the square in Table II.

One might hope that with other groups more than r = minimum $p_i^{e_i} - 1$ orthogonal squares might be obtained. It has been shown however that using any group and its automorphisms at most r orthogonal squares can be obtained.

A more general method based on groups is given in a recent paper (H. B. Mann, "The construction of sets of orthogonal Latin squares," *Annals of Math. Stat.*, Vol. 13 (1942)). It can be shown that also with this more general method no $4n + 2$ sided Graeco-Latin square can be constructed.

ADDITIONAL LITERATURE

R. C. Bose: "On the application of the properties of Galois-fields to the construction of completely orthogonalized Latin squares," *Sankhyā*, 1939.
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ON THE DEPENDENCE OF SAMPLING INSPECTION PLANS UPON POPULATION DISTRIBUTIONS

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1. Introduction. The foundations of the science of quality control and quality determination have been laid by W. A. Shewhart [1, 2]. His ideas pervade what follows, but they are too well known to require discussion here. There is, however, one that should be specifically mentioned, that of *statistically controlled production*, because it provides the justification for the basic assumption of this paper: *When production is statistically controlled, there exists a probability, $P(N, X)$, that a lot of size N will contain X defective items.* Shewhart has given a complete discussion of assumptions of this nature.

Sampling inspection of lots may take one of two courses:

(a) Item inspection, in which a lot is accepted or completely inspected on the basis of one or more samples drawn from the lot.

(b) Lot inspection, in which a lot is accepted or rejected on the basis of one or more samples drawn from the lot.

The former has been extensively studied by Dodge and Romig [3, 4, 5]; the latter has received little attention, but some of the basic ideas of Dodge and Romig are applicable to this case also.

In this paper the approach to the general problem of lot inspection will be different from that of Dodge and Romig in one important respect: The role of the population distribution function will be emphasized, whereas they have directed their attention to methods which require no knowledge of the population distribution. Their techniques are particularly valuable when a probability distribution does not exist, that is, when production is not statistically controlled. The interest here will be in the inspection of lots which may be regarded as having been drawn from a statistical population. After the first sample from the first lot has been drawn, something is known of the distribution of that population, and as the inspection proceeds a great body of knowledge may be accumulated. Here, if ever, is a real opportunity to explore and to use a population distribution. The very nature of inspection supplies a continuous flow of information about it. To neglect this information would be wasteful indeed.

It is, therefore, the object of this paper to point the way to more efficient inspection procedures for situations in which production is statistically controlled. The inspection procedure will be considered to be an inferential process—on the basis of one or more samples, and with whatever information is available about the parent distribution, an inference will be made regarding the quality

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of those items which have not been examined. A distinction is made between the original lot and what remains of the lot after samples have been drawn. The latter is the appropriate subject of the inference, inasmuch as the quality of the sample is exactly known. The importance of this distinction will become clear in the third section of the paper.

The subject is, unhappily, very briefly developed. The paper contains a few fundamental results and some suggested proceedures that may be used to obtain results of more immediate practical value. Time and facilities were not available for preparation of specific sampling plans.

2. Notation and formulae. The conventional notations $P(u)$, $P(u \mid v)$, $P(u, v)$ will be used to denote the probability of u, of u given v, of u and v, respectively. A lot will contain N items of which X are defective. A lot from which one sample has been drawn will be called an "x-lot;" after i samples have been drawn it will be referred to as an "x^i-lot." The number of items in the i-th sample will be n_i of which x_i are defective, except that the subscript will often be omitted when $i = 1$. The number of items in an x^k-lot will be:

$$N_k = N - \sum_{i=1}^{k} n_i$$

of which

$$X_k = X - \sum_{i=1}^{k} x_i$$

are defective.

The probability of x_i for a given x^{i-1}-lot is:

$$P(x_i \mid X_{i-1}) = \binom{n_i}{x_i} X_{i-1}^{(x_i)} (N_{i-1} - X_{i-1})^{(n_i - x_i)} / N_{i-1}^{(n_i)}, \tag{1}$$

where $\binom{u}{v}$ is the binomial coefficient, and

$$u^{(v)} = u(u-1)(u-2)\cdots(u-v+1).$$

Under this conditional distribution, the m-th factorial moment of x_i is:

$$E(x_i^{(m)} \mid X_{i-1}) = n_i^{(m)} X_{i-1}^{(m)} / N_{i-1}^{(m)}, \tag{2}$$

and the m-th factorial moment of X_i is:

$$E(X_i^{(m)} \mid X_{i-1}) = N_i^{(m)} X_{i-1}^{(m)} / N_{i-1}^{(m)}. \tag{3}$$

Repeated application of (3) to (2) results in:

$$E(x_i^{(m)}) = n_i^{(m)} E(X^{(m)}) / N^{(m)}. \tag{4}$$

In similar fashion it may be shown that:

$$E\left(\prod_{i=1}^{k} x_i^{(m_i)}\right) = \prod_{i=1}^{k} n_i^{(m_i)} E(X^{(\Sigma m)}) / N^{(\Sigma m_i)}. \tag{5}$$

3. Single sampling. Consider a population of lots of fixed size N such that the probability that a lot will contain X defective items is $P(X)$. If x is the number of defective items in a sample of size n drawn from one of these lots, then the joint probability of x and X is:

$$P(x, X) = \binom{n}{x} \frac{X^{(x)}(N - X)^{(n-x)}}{N^{(n)}} P(X). \tag{6}$$

The fundamental result of this paper is:

THEOREM 1. *The correlation between the number of defective items in the sample, x, and the number of defective items in the remainder of the lot, $X_1 = X - x$, is positive, zero, or negative according as the variance, σ_X^2, of X is greater than, equal to, or less than $A - A^2/N$, where A represents the expected value of X.*

To prove this statement, one need merely compute the covariance between x and X_1:

$$r_{xX_1}\sigma_x\sigma_{X_1} = \sum_{x,X} x(X - x)P(x, X) - E(x)(A - E(x)). \tag{7}$$

Summing first on x with the aid of (2):

$$r_{xX_1}\,\sigma_x\,\sigma_{X_1} = \sum_X \left(\frac{n}{N} X^2 - \frac{n^{(2)}}{N^{(2)}} X^{(2)} - \frac{n}{N} X\right)P(X) - E(x)(A - E(x))$$

which may be reduced to:

$$r_{xX_1}\,\sigma_x\,\sigma_{X_1} = \frac{n(N - n)}{N(N - 1)}\left[\sigma_X^2 - \left(A - \frac{A^2}{N}\right)\right] \tag{8}$$

by employing the definitions of A and σ_X^2 together with the relation,

$$E(x) = nA/N,$$

which follows from (4) on putting $m = 1$.

The fact that $A - A^2/N$ is the variance of a binomial distribution with mean A and range N, suggests:

THEOREM 2. *If X has the binomial distribution,*

$$P(X) = \binom{N}{X} p^X(1 - p)^{N-X}, \tag{9}$$

then x and $X - x$ are independently distributed.

This statement is readily verified by substituting (9) in (6), and X_1 for $X - x$; a rearrangement of factors then gives:

$$P(x, X_1) = \left[\binom{n}{x} p^x(1 - p)^{n-x}\right]\left[\binom{N - n}{X_1} p^{X_1}(1 - p)^{N-n-X_1}\right].$$

It is clear that additional samples drawn from such lots will have the same property. Thus, sampling of lots drawn from a binomial population will provide no basis whatsoever for inferences concerning the remainder of the lot.

The question naturally arises as to whether distributions $P(X)$ exist for which $r_{xx_1} = \pm 1$.

THEOREM 3. *If*

$$\begin{aligned} P(X) &= 1, \quad X = A, \quad A \neq 0 \text{ or } N \\ &= 0, \quad X \neq A, \end{aligned} \tag{10}$$

then $r_{xx_1} = -1$; *if*

$$\begin{aligned} P(X) &= p, \quad X = 0 \\ &= 1 - p, \quad X = N \\ &= 0, \quad X = 1, 2, \cdots, N-1, \end{aligned} \tag{11}$$

then $r_{xx_1} = 1$. *These are the only distributions which lead to these values of* r_{xx_1}. It is first necessary to compute

$$\sigma_x^2 = \frac{n^{(2)}}{N^{(2)}}\left[\sigma_X^2 + \frac{N-n}{n-1}\left(A - \frac{A^2}{N}\right)\right] \tag{12}$$

$$\sigma_{x_1}^2 = \frac{(N-n)^{(2)}}{N^{(2)}}\left[\sigma_X^2 + \frac{n}{N-n-1}\left(A - \frac{A^2}{N}\right)\right] \tag{13}$$

by means of (2), (3), and (4). These, together with (8), may then be used to reduce the condition, $r_{xx_1}^2 = 1$, to the following condition on $P(X)$: either

$$\sum_X (X - A)^2 P(X) = 0, \tag{14}$$

or

$$\sum_X X(N - X)P(X) = 0, \tag{15}$$

whence the theorem follows at once. The distributions defined by (10) and (11) will be referred to hereafter as $P_-(X)$ and $P_+(X)$ respectively.

THEOREM 4. *The correlation,* r_{xX}, *between* x *and* X *is positive unless* X *is distributed by* $P_-(X)$ *in which case it is zero.*

Computing the covariance by means of (2), (3), and (4), one finds that

$$r_{xX}\sigma_x\sigma_X = n\sigma_X^2/N. \tag{16}$$

The reason for so carefully distinguishing between the x-lot and the original lot is now apparent. While the number of defective items in the sample is always positively correlated with the number of defective items in the original lot (Theorem 4), it may be negatively correlated with the number of defective items in the x-lot (Theorem 1). The normal practice is to reject (or completely inspect) the x-lot if the sample has an excessive number of defectives, but when the distribution is sharper than a binomial distribution ($\sigma_X^2 < A - A^2/N$) just the reverse should be done. It is assumed, of course, that defective items would be removed from the sample during its inspection when the inspection was nondestructive.

It is clear that the basic rationale of a sampling inspection plan depends on the condition of Theorem 1. Having chosen a sample size n and an acceptance number a (defined by Dodge and Romig [1]), an x-lot would be

Accepted when $x \leq a$ if $\sigma_X^2 > A - A^2/N$

Rejected when $x > a$ if $\sigma_X^2 > A - A^2/N$

but

Accepted when $x > a$ if $\sigma_X^2 < A - A^2/N$

Rejected when $x \leq a$ if $\sigma_X^2 < A - A^2/N$.

Thus, it is essential that the first two moments of the population distribution be known accurately enough to determine the sign of $\sigma_X^2 - (A - A^2/N)$ before an efficient inspection plan can be devised.

4. Multiple sampling. In this section are given similar criteria for guidance in formulating more elaborate sampling plans. The actual computations are elementary and will be omitted.

THEOREM 5. *The mean and variance of the number of defective items in a sample drawn from an x^i-lot are*:

$$E(x_i) = n_i A/N \tag{17}$$

$$\sigma_{x_i}^2 = \frac{n_i^{(2)}}{N^{(2)}}\left[\sigma_X^2 + \frac{N - n_i}{n_i - 1}\left(A - \frac{A^2}{N}\right)\right]. \tag{18}$$

THEOREM 6. *The mean and variance of the number of defective items in an x^i-lot are*:

$$E(X_i) = N_i A/N \tag{19}$$

$$\sigma_{X_i}^2 = \frac{N_i^{(2)}}{N^{(2)}}\left[\sigma_X^2 + \frac{N - N_i}{N_i - 1}\left(A - \frac{A^2}{N}\right)\right]. \tag{20}$$

THEOREM 7. *The correlation between the numbers of defective items in the i-th and j-th samples is*:

$$r_{x_i x_j} = \frac{1}{\sigma_{x_i}\sigma_{x_j}}\frac{n_i n_j}{N^{(2)}}\left[\sigma_X^2 - \left(A - \frac{A^2}{N}\right)\right]. \tag{21}$$

THEOREM 8. *The correlation between the numbers of defective items in the i-th sample and the x^j-lot is given by*:

$$r_{x_i X_j}\sigma_{x_i}\sigma_{X_j} = \frac{n_i(N_j - 1)}{N^{(2)}}\left[\sigma_X^2 + \frac{N - N_j}{N_j - 1}\left(A - \frac{A^2}{N}\right)\right], \qquad i > j \tag{22}$$

$$= \frac{n_i N_j}{N^{(2)}}\left[\sigma_X^2 - \left(A - \frac{A^2}{N}\right)\right], \qquad i \leq j. \tag{23}$$

Thus, the correlation is always positive if the sample is part of the lot even when X has the distribution $P_-(X)$, except only the case covered by Theorem 4 when $j = 0$. The correlations (21) and (23) will be positive or negative in accordance

with the condition of Theorem 1. The extreme values of all these correlations are again given by the distributions $P_-(X)$ and $P_+(X)$ defined in Theorem 3. When $P(X) = P_+(X)$, they all become plus one; when $P(X) = P_-(X)$, they become:

$$r_{z_i z_j} = -\sqrt{n_i n_j/(N - n_i)(N - n_j)}, \tag{24}$$

$$r_{z_i x_j} = \sqrt{n_i(N - N_j)/N_j(N - n_i)}, \qquad i > j \tag{25}$$

$$= -\sqrt{n_i N_j/(N - n_i)(N - N_j)}, \qquad i \leq j \tag{26}$$

For $i = j = 1$, this last expression becomes minus one in accordance with Theorem 3.

5. Formulation of inspection plans. In practice, the formulation of specific sampling inspection plans would naturally begin with the examination of a preliminary sample (or samples) in order to estimate the first two moments of the population distribution. It would then be convenient to have some simple standard functional form which could be fitted to the distribution by means of these first two moments. Such a standard form must obviously contain two arbitrary parameters and should represent a discrete distribution with range N. The simplest function known to the author which satisfies these conditions is:

$$P_1(X) = \binom{N}{X} C^{(X)} D^{(N-X)}/(C + D)^{(N)}. \tag{27}$$

But it will be seen that this distribution is always sharper than the binomial distribution with the same range and mean. Hence a second form is suggested,

$$P_2(X) = \binom{N}{X} (C + X)^{(X)}(D + N - X)^{(N-X)}/(C + D + N + 1)^{(N)}, \tag{28}$$

which, it turns out, is always flatter than the binomial distribution with the same range and mean. It is proposed that these two functions be used as standard forms in the belief that the simplicity of their functional form is a convenience which outweighs the inconvenience of having to study two separate functions.

The factorial moments of these distributions are:

$$\sum_0^N X^{(m)} P_1(X) = N^{(m)} C^{(m)}/(C + D)^{(m)} \tag{29}$$

$$\sum_0^N X^{(m)} P_2(X) = N^{(m)}(C + m)^{(m)}/(C + D + m + 1)^{(m)} \tag{30}$$

The variances are:

$$\sum_0^N (X - A)^2 P_1(X) = \frac{NCD(C + D - N)}{(C + D)^2(C + D - 1)} \tag{31}$$

$$\sum_0^N (X - A)^2 P_2(X) = \frac{N(C + 1)(D + 1)(N + C + D + 2)}{(C + D + 2)^2(C + D + 3)} \tag{32}$$

Examination of the expression, $\sigma_X^2 - (A - A^2/N)$, reveals that for $P_1(X)$ it is always negative, while for $P_2(X)$ it is always positive. Both $P_1(X)$ and $P_2(X)$ approach the binomial distribution when C and D become large in a fixed ratio. $P_1(X)$ becomes $P_{-}(X)$ when $C = A$ and $D = N - A$. As C and D become larger, the distribution becomes flatter until in the limit it is the binomial distribution. $P_2(X)$ becomes the rectangular distribution, $P(X) = 1/(N + 1)$, when $C = D = 0$, and becomes sharper as C and D increase.

The two distribution functions will not serve to approximate U-shaped distributions, and $P_1(X)$ has the disadvantage that C and D must be integers when they are less than N if negative probabilities are to be avoided, but since $C + D$ will be greater than or equal to N in any case, and much greater than N in most cases, this is not a serious limitation. The two functions are reproduced when the marginal distributions for samples are computed:

$$P_1(x_i) = \sum_{X,x_1,\cdots,x_{i-1}} P(x_1, \cdots, x_i \mid X)P_1(X)$$

$$= \binom{n_i}{x_i} C^{(x_i)} D^{(n_i - x_i)}/(C + D)^{(n_i)} \tag{33}$$

$$P_2(x_i) = \sum_{X,x_1,\cdots,x_{i-1}} P(x_1, \cdots, x_i \mid X)P_2(X)$$

$$= \binom{n_i}{x_i} (C + x_i)^{(x_i)}(D + n_i - x_i)^{(n_i - x_i)}/(C + D + n_i + 1)^{(n_i)}. \tag{34}$$

This is a most valuable property for two reasons. In the first place, it will appreciably facilitate the tedious machine calculations necessary in the work of providing specific optimum sampling plans. In the second place, it will simplify the study of the population distribution of lots by means of samples from those lots.

These two distributions should, then, provide an adequate basis for the formulation of sampling inspection plans in most circumstances.

6. Efficiency of sampling inspection. There are two aspects to the efficiency of an item inspection plan: the inspection aspect, which would be measured by the proportion of defective items eliminated, and the sampling aspect, which would be measured by the difference between the proportions of defective and good items examined. These two measures are primarily functions of the amount of inspection; the former will be large when the amount of inspection is large, and the latter will ordinarily be large when the amount of inspection is small. They will not, therefore, serve as useful criteria for excellence. The measure to be used here is:

$$E = R_B - R_G \tag{35}$$

where R_B is the proportion of defective items examined, and R_G is the proportion of good items examined. It will be zero when the inspection plan is not at all selective, and will be 100% when all of the defective items and none of the good

items are examined. It measures both aspects mentioned above, but has the disadvantage that it emphasizes one or the other for different amounts of inspection. It is not, therefore, a particularly good measure of efficiency, but it is a good criterion. It should ordinarily be maximized.

For single sampling with an acceptance number, a, and with a population distribution sharper than the binomial, the number of items inspected on the average per lot is:

$$I = n + (N - n) \sum_0^a P(x) \tag{36}$$

and the number of defective items inspected on the average per lot is:

$$B = E(x) + \sum_0^N \sum_0^a (X - x)P(x, X) \tag{37}$$

The efficiency will be:

$$E = B/A - (I - B)/(N - A) \tag{38}$$

which may be put in the form:

$$E = \frac{N(N-n)}{A(N-A)} \sum_0^N \sum_0^a \left(\frac{X-x}{N-n} - \frac{A}{N}\right)P(x, X) \tag{39}$$

after substituting (36) and (37). This may be further simplified to:

$$E = \frac{N(N-n)}{A(N-A)} \sum_0^a \left[\frac{x+1}{n+1} P_{n+1}(x) - \frac{A}{N} P_n(x)\right], \tag{40}$$

where $P_m(x)$ is the marginal distribution of x for samples of size m. For distributions flatter than the binomial, the limits of the summations on x would be $a + 1$ to n throughout, instead of 0 to a.

THEOREM 9. *For a fixed value of n, the acceptance number which maximizes E is $a = E(x)$ when X is distributed by $P_1(X)$ or $P_2(X)$.*

The expression in the brackets of (40) becomes:

$$\frac{E(x) - x}{C + D - n} P_n(x) \tag{41}$$

when (33) is substituted for $P(x)$, and becomes:

$$\frac{x - E(x)}{C + D + n + 2} P_n(x) \tag{42}$$

when (34) is substituted for $P(x)$. This theorem is true for a wider class of distribution functions, $P(X)$, but is not worth pursuing too deeply because its main value is in the light it throws on the general nature of inspection plans. It will be a rare case in practice when n is fixed and a is unrestricted. Some idea of the manner in which E depends on population distributions can be attained by computing it for some simple distributions, and by examination of equation (40).

E can be 100% only when all submitted items are defective, but it will obviously be very near 100% when the distribution is $P_+(X)$ if samples of one are used. However, a more reasonable maximum might be 50% which is the largest possible value when the distribution is rectangular (as is shown in the next section). As the distribution becomes sharper, the maximum efficiency decreases to zero when the binomial distribution is reached. As the distribution becomes still sharper, the efficiency increases until it again reaches 50% for the distribution $P_-(X)$. Thus the efficiency is limited, and, in fact, will ordinarily be further reduced by conditions (fixed amount of inspection, or fixed outgoing quality level, for example) which will not allow the unrestricted maximum efficiency to be used.

7. Sampling plans for the rectangular distribution. Excluding the extreme distributions, $P_-(X)$ and $P_+(X)$, the distribution which provides the simplest illustration of some of the ideas above is the rectangular one:

$$P(X) = 1/(N+1), \qquad X = 0, 1, 2, \cdots, N, \tag{43}$$

the mean and variance of which are:

$$A = N/2$$
$$\sigma_X^2 = N(N+2)/12. \tag{44}$$

The marginal distribution of x is:

$$P(x) = 1/(n+1), \tag{45}$$

and the efficiency is:

$$E = 2\frac{(N-n)(n-a)(a+1)}{N(n+1)(n+2)}. \tag{46}$$

The values of n and a which maximize this expression are:

$$n = \sqrt{N+2} - 2$$
$$a = (\sqrt{N+2} - 3)/2 \tag{47}$$

whence

$$E_{\max} = \frac{1}{2}\left(1 - \frac{1}{\sqrt{N+2}}\right)\left(1 - \frac{\sqrt{N+2}-2}{N}\right), \tag{48}$$

or nearly 50% for large N. This plan eliminates almost 75% of the defective items and entails examination of about 25% of the good items. 50% of all items will be inspected.

If the proportion of items to be inspected is fixed at r, then the maximization of E is subject to the restriction:

$$rN = n + (N-n)(n-a)/(n+1) \tag{49}$$

and results in:

$$(50)\quad n = \frac{-nN(2-r) + \sqrt{n^2N^2(2-r)^2 + N(rN+2r-2)(N-Nr-1)}}{N(1-r)-1}$$

or for large N,

$$(51)\quad \begin{aligned} n &= \sqrt{rN/(1-r)} \\ a &= \sqrt{r(1-r)N}. \end{aligned}$$

If the average outgoing quality (as defined by Dodge and Romig) is to be fixed at p (the proportion of defectives after inspection on the average), then the maximization of E is subject to the condition:

$$(52)\quad p = \frac{(N-n)(a+2)^{(2)}}{N(n+2)^{(2)} + (N-n)(a+2)^{(2)}}$$

and results in the relation:

$$(53)\quad (N-n)(n-a) = (a+1)(n+1)(n+2).$$

When N is large relative to $1/p$, the solution of these last two equations is approximately:

$$(54)\quad \begin{aligned} n &= \sqrt{N}\sqrt{\sqrt{\frac{1-p}{p}} - 1} \\ a &= \sqrt{\frac{p}{1-p}}\, n. \end{aligned}$$

The same result would have been obtained had the amount of inspection been minimized subject to (52).

8. Summary. Methods of sampling inspection in current use have been made independent of any population distribution that may exist. When production is statistically controlled, a population distribution may be postulated. In such circumstances it is to be expected that knowledge gained of the population by repeated sampling will be a valuable aid in specifying efficient sampling inspection techniques. This paper is a preliminary investigation of the relation of lot sampling inspection plans to population distributions.

Lots are assumed to be drawn from a population such that there is a unique probability the lot will contain a specified number of defective items. It is shown that:

1. The number of defective items in a sample from a lot is positively or negatively correlated with the number of defective items in the remainder of the lot according as the population distribution is "flatter" than or "sharper" than a binomial distribution. Distributions are found for which this correlation is plus or minus one.

2. If the distribution is the binomial one, the number of defective items in the sample is distributed independently of the number of defective items in the remainder of the lot. Thus a sample can furnish no basis for an inference concerning the remainder of the lot.
3. The correlation between the number of defective items in the sample and the number of defective items in the original lot is positive.

These results are generalized for repeated sampling of one lot.

There is discussed a standard functional form which can ordinarily be fitted to population distribution functions for purposes of constructing sampling inspection plans.

It is shown, for a class of distribution functions, that a single sampling plan for nondestructive inspection will be most efficient in a certain sense when the acceptance number is equal to the expected number of defective items in the sample.

Optimum single sampling plans for nondestructive inspection of lots with a rectangular probability distribution are determined for restricted amount of inspection and for restricted average outgoing quality.

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ON CARD MATCHING

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1. Introduction. Several authors have discussed the probability of obtaining a given number of matched pairs of cards under conditions of random pairing of two decks of arbitrary composition. The exact expression for this probability (equation (6)) is ordinarily too complicated for use in computing significance levels. This is especially true for certain practical applications. For example, in a square two-way contingency table in which the categories corresponding to rows are identical with those for columns, the sum of the entries in the diagonal cells has this distribution. Intuitively one would suspect that the distribution is asymptotically normal, as suggested by several authors. In the following section proof is given that the number of matched cards is asymptotically normally distributed when the total number of cards in each of the two decks approaches infinity with the proportion of cards in each suit of each deck remaining fixed. The form of the limiting distribution can then be used in computing approximate significance levels.

A problem of some interest to psychologists is that of determining whether an individual has matched two series of items better than could have been done "by chance"; for instance, whether a graphologist has matched personality descriptions with specimens of handwriting better than by chance. The problem can also be phrased in terms of card matching under random pairing of two identical decks each of a given number of different cards. This will be recognized as a classical problem of probability theory: Let tickets numbered from 1 to n be placed in a hat. If the tickets are drawn one by one from the hat, what is the probability that the number of the drawing will coincide with the number drawn a specified number of times? It is clear how the analagous problem of matching cards of three or more identical decks of a given number of different cards arises (e.g., matching appearance, personality, and handwriting). The latter part of the present paper is concerned with this problem. Battin [1] has displayed a generating function for the probability of obtaining a given number of matched cards between any number of decks of arbitrary composition. Battin's generating function is used to derive explicitly the probability of obtaining a specified number of matched cards and the moments of the distribution.

2. The Limiting Distribution of the Number of Matched Cards. In the ordinary card matching problem one is interested in the number of matchings when two decks, say D_1 and D_2, are paired randomly. Let D_1 consist of n_{11}, n_{12}, $\cdots$, n_{1k} cards of suits S_1, S_2, $\cdots$, S_k, respectively, and let D_2 consist of n_{21}, n_{22}, $\cdots$, n_{2k} cards of suits S_1, S_2, $\cdots$, S_k, respectively (any n_{ai} can be 0), where

$$\sum_{i=1}^{k} n_{1i} = \sum_{i=1}^{k} n_{2i} = n.$$

Let t_{ij} $(i, j = 1, 2, \cdots, k)$ be the number of pairings each involving a card from D_1 of suit S_i and a card from D_2 of suit S_j. It is easily seen that the probability of a set $|| t_{ij} ||$ under random pairing is the same as that associated with the entries $|| t_{ij} ||$ in a k by k contingency table [2] for which the row totals are fixed as $n_{11}, n_{12}, \cdots, n_{1k}$, and the column totals are fixed as $n_{21}, n_{22}, \cdots, n_{2k}$, i.e.

$$P(t_{ij}) = \frac{\prod_{i=1}^{k} n_{1i}! \prod_{j=1}^{k} n_{2j}!}{n! \prod_{i,j=1}^{k} t_{ij}!}. \tag{1}$$

The probability of obtaining h matchings is the same as that of the sum of diagonal terms in a square contingency table, i.e., $h = \sum_{i=1}^{k} t_{ii}$. In fact, in practical cases, the problem frequently arises in this manner: If two individuals each classify n objects into k categories, h is the number of objects on whose classification they agree.

The distribution (1) has essentially $(k-1)^2$ variables since there are $2k-1$ linear restrictions imposed on the t_{ij}. It is easy to verify that, for fixed $n_{1i}/n = m_{1i}$, say, and fixed $n_{2i}/n = m_{2i}$, say, the distribution (1) approaches the normal distribution in $(k-1)^2$ linearly independent variables, as n approaches infinity. Let us substitute

$$x_{ij} = \frac{t_{ij} - n m_{1i} m_{2j}}{\sqrt{n}} \qquad (i, j = 1, 2, \cdots, k),$$

use Stirling's formula for each factorial in (1), and take the logarithm. The argument proceeds in a manner similar to the classical case of the limit of the binomial distribution.

Since there are imposed linear restrictions on the t_{ij}

$$\sum_{j=1}^{k} t_{ij} = n \cdot m_{1i} \qquad (i = 1, 2, \cdots, k),$$

$$\sum_{i=1}^{k} t_{ij} = n \cdot m_{2j} \qquad (j = 1, 2, \cdots, k),$$

there are also restrictions on the x_{ij}, namely,

$$\sum_{j=1}^{k} x_{ij} = \sum_{i=1}^{k} x_{ij} = 0.$$

Hence there are $(k-1)^2$ linearly independent x_{ij}. If we choose x_{ij} $(i, j = 1, 2, \cdots, k-1)$ as the linearly independent variables, the limiting probability element as n approaches infinity, is

$$\frac{1}{(2\pi)^{\frac{1}{2}(k-1)^2} \left(\prod_{i=1}^{k} m_{1i} \prod_{j=1}^{k} m_{2j} \right)^{\frac{1}{2}(k-1)}} e^{-\frac{1}{2}Q} \prod_{i,j=1}^{k-1} dx_{ij}, \tag{2}$$

where

$$Q \doteq \sum_{i,j=1}^{k} \frac{x_{ij}^2}{m_{1i} m_{2j}}$$

is written in terms of all the x_{ij} with the understanding that the linearly depenent variables are linear functions of the independent variables.

Now $h - E(h)$ is simply a linear combination of x_{ij}, namely,

$$h - E(h) = \sqrt{n} \sum_{i=1}^{k} x_{ii}.$$

Hence, it follows that

$$\frac{h - E(h)}{\sqrt{n}\,\sigma_h}$$

is asymptotically normally distributed with mean zero and variance unity. For large n, then, it is possible to use the normal distribution to approximate significance levels for h.

Of course, any other linear combination of the entries t_{ij} is asymptotically normally distributed. The quantity Q in (2) can be recognized as the Pearson χ^2 for contingency tables, and the above constitutes proof that it actually has the χ^2 distribution with $(k-1)^2$ degrees of freedom.

3. Matchings between three or more decks. There are instances, such as the classification of n objects into k categories by 3 or more individuals, in which one is interested in the matchings of three decks or more. For any number of decks one can prove in a manner exactly analagous to §2 that the distribution of the number of matchings is asymptotically normal. Here the demonstration is indicated for three decks. Let us consider three decks D_α ($\alpha = 1, 2, 3$) with $n_{\alpha 1}, n_{\alpha 2}, \cdots, n_{\alpha k}$, cards of suits $S_1, S_2, \cdots, S_k$, respectively. Let t_{gij} be the number of triplets consisting of a card from S_g of D_1, a card from S_i of D_2, and a card from S_j of D_3 under random formation of triplets (i.e., laying down the three shuffled decks side by side).

The probability law of the set $\{t_{gij}\}$ can be derived by the consideration of the generating function,

$$(x_1 y_1 z_1 + x_1 y_1 z_2 + \cdots + x_1 y_2 z_1 + \cdots + x_2 y_1 z_1 + \cdots + x_k y_k z_k)^n$$

$$= \sum \frac{n!}{\prod_{g,i,j} t_{gij}!} \prod_{g,i,j} (x_g y_i z_j)^{t_{gij}}, \tag{3}$$

where the summation extends over all the partitions $\{t_{gij}\}$ of n. The number of ways of deriving the set $\{t_{gij}\}$ is the coefficient of $\prod_{g,i,j} (x_g y_i z_j)^{t_{gij}}$, namely,

$$\frac{n!}{\prod_{g,i,j} t_{gij}!},$$

where $\sum_{i,j} t_{gij} = n_{1g}$, $\sum_{g,j} t_{gij} = n_{2i}$, and $\sum_{g,i} t_{gij} = n_{3j}$.

The total number of ways of getting the marginal totals n_{1g}, n_{2i}, and n_{3j} is the coefficient of $\prod_{g,i,j} x_g^{n_{1g}} y_i^{n_{2i}} z_j^{n_{3j}}$ in (3); that is, in

$$\left(\sum_{g,i,j} x_g y_i z_j\right)^n = \left(\sum_g x_g\right)^n \left(\sum_i y_i\right)^n \left(\sum_j z_j\right)^n$$

$$= \sum_{g,i,j} \frac{n!}{\prod_g n_{1g}!} \cdot \frac{n!}{\prod_i n_{2i}!} \cdot \frac{n!}{\prod_j n_{3j}!} x_g^{n_{1g}} y_i^{n_{2i}} z_j^{n_{3j}}.$$

The probability of getting the set $\{t_{gij}\}$ is the ratio of these expressions,

$$P(t_{gij}) = \frac{n!}{\prod_{g,i,j} t_{gij}!} \Big/ \left[\frac{n!}{\prod_g n_{1g}!} \cdot \frac{n!}{\prod_i n_{2i}!} \cdot \frac{n!}{\prod_j n_{3j}!}\right]$$

$$= \frac{\prod_g n_{1g}! \cdot \prod_i n_{2i}! \cdot \prod_j n_{3j}!}{(n!)^2 \prod_{g,i,j} t_{gij}!} \tag{4}$$

This formula is analagous to (1) and, indeed, reduces to (1) for $n_{31} = n$, $n_{3j} = 0$ ($j = 2, 3, \cdots, k$). This is the probability associated with a three-way contingency table (k by k by k). For a contingency table, k by l by m, this probability would be (4) with the limits on g of 0 and k; on i, 0 and l; and on j, 0 and m.

For fixed values of the ratios $n_{\alpha i}/n = m_{\alpha i}$ ($\alpha = 1, 2, 3$; $i = 1, 2, \cdots, k$), say, the $k^3 - 3k + 2$ linearly independent variates in the set $\{t_{gij}\}$ are asymptotically normally distributed. To demonstrate this, substitute

$$x_{gij} = \frac{t_{gij} - n m_{1g} m_{2i} m_{3j}}{\sqrt{n}} \qquad (g, i, j = 1, 2, \cdots, k)$$

into (4) and use Stirling's approximation. There are $3k - 2$ independent linear restrictions on the x_{gij}, namely,

$$\sum_{i,j=1}^{k} x_{gij} = \sum_{g,j=1}^{k} x_{gij} = \sum_{g,i=1}^{k} x_{gij} = 0.$$

Therefore, there are $k^3 - 3k + 2$ x's which are unrestricted. Using these variables, we find that the limiting probability element of these x_{gij} is

$$\frac{1}{(2\pi)^{\frac{1}{2}(k^3-3k+2)} \left(\prod_g m_{1g} \prod_i m_{2i} \prod_j m_{3j}\right)^{\frac{1}{2}(k^2-1)}} e^{-\frac{1}{2}Q} \prod dx_{gij}, \tag{5}$$

where

$$Q = \sum_{g,i,j=1}^{k} \frac{x_{gij}^2}{m_{1g} m_{2i} m_{3j}},$$

and the product of differentials is of $k^3 - 3k + 2$ variables. The number of matched triplets u, say, is the sum $\sum_{i=1}^{k} t_{iii}$, and we have

$$\frac{u - E(u)}{\sqrt{n}} = \sum_{i=1}^{k} x_{iii}.$$

From these facts it follows that $\frac{u - E(u)}{\sqrt{n}}$ is asymptotically normally distributed.

The above results may be easily generalized. In a q-way contingency table with fixed marginal totals $n \cdot m_{\alpha i}$ ($\alpha = 1, 2, \cdots, q$; $i = 1, 2, \cdots, k$), the probability of a set $\{t_{gi \cdots j}\}$ is

$$\frac{\prod_{\alpha=1}^{q} \prod_{i=1}^{k} (n \cdot m_{\alpha i})!}{(n!)^{q-1} \prod_{g,i,\cdots,j=1}^{k} t_{gi \cdots j}!}.$$

The entries minus their respective means and divided by $\sqrt{n}$, namely,

$$x_{gi \cdots j} = \frac{t_{gi \cdots j} - n m_{1g} m_{2i} \cdots m_{qj}}{\sqrt{n}}$$

are asymptotically normally distributed according to

$$(2\pi)^{-\frac{1}{2}(k^q - qk + q - 1)} \left(\prod_{\alpha=1}^{q} \prod_{i=1}^{k} m_{\alpha i} \right)^{-\frac{1}{2}(k^{q-1} - 1)} e^{-\frac{1}{2}Q},$$

where

$$Q = \sum_{g,i,\cdots,j=1}^{k} \frac{x_{gi \cdots j}^2}{m_{1g} m_{2i} \cdots m_{qj}}.$$

The generalization of Pearson's χ^2, namely Q, has the χ^2-distribution with $k^q - qk + q - 1$ degrees of freedom. Finally,

$$s = \sum_{i=1}^{k} t_{ii \cdots i},$$

the number of matched q-tuplets, under random formation of q-tuplets is asymptotically normally distributed.

4. Matching cards of identical decks, each of n different cards. The probability of obtaining a given number of pairs of matched cards under random pairing of two identical decks each of n different cards has been derived by Chapman [3] by a straightforward method and, of course, the solution of the classical problem mentioned in the introduction is this probability. Another technique involving the use of the general expression for the number of matchings of two decks of arbitrary composition can be easily generalized to three or more decks.

Before discussing this method, let us derive this general expression first by the use of the generating function discussed by Battin. Consider the multinomial

$$(x_1y_1e^{\theta} + x_1y_2 + \cdots + x_2y_1 + x_2y_2e^{\theta} + \cdots + x_ky_ke^{\theta})^n.$$

The coefficient of $e^{h\theta}x_1^{n_{11}} \cdots x_k^{n_{1k}}y_1^{n_{21}} \cdots y_k^{n_{2k}}$ (where k is the number of suits; n_{1i} the number of cards of suit S_i in the first deck; n_{2i} the number of cards of suit S_i in the second deck; and $n = \Sigma n_{1i} = \Sigma n_{2i}$) is the number of ways the cards may be arranged so that there are h matchings. After expanding the multinomial

$$[\sum_i x_iy_ie^{\theta} + (\sum_i x_i)(\sum_j y_j) - \sum_i x_iy_i]^n$$

in powers of x_i and y_i, taking the proper coefficient, and dividing by the total number of ways the cards can be arranged, one arrives at the probability law of h [4],

$$P(h) = \frac{\prod_i n_{1i}! \prod_j n_{2j}!}{(n!)^2} \sum_{g=0}^{n-h} (-1)^{n-h-g} \binom{n}{h}\binom{n-h}{g} T_g, \tag{6}$$

where

$$T_g = \sum \frac{(g!)^2(n-g)!}{\prod_{i=1}^{k} [(n_{1i}-s_i)!\,(n_{2i}-s_i)!\,s_i!]}, \tag{7}$$

where the summation is extended over all s_i, satisfying the following conditions:

$$\Sigma s_i = n - g, \qquad n_{1i} - s_i \geq 0, \qquad n_{2i} - s_i \geq 0, \qquad s_i \geq 0$$
$$(i = 1, 2, \cdots, k).$$

From (6) one can easily derive the distribution of the number of matchings when two identical decks of n different cards are randomly paired. Let $n_{1i} = 1$, $n_{2i} = 1$, and $n = k$. Then T_g as defined in (7) is

$$T_g = \sum \frac{(g!)^2(n-g)!}{(0!0!1!)^{n-g}(1!1!0!)^g} = \frac{n!}{g!(n-g)!}(g!)^2(n-g)!$$

for s_i can equal 0 or 1 and there are ${}_nC_g$ choices of the 0's. Hence, we find the probability of the number of matchings v to be

$$P(v) = \frac{1}{v!} \sum_{j=0}^{n-v} \frac{(-1)^j}{j!}. \tag{8}$$

This result has been given by Chapman [3]. It is, in fact, a classical probability law.

The moment generating function is

$$\varphi(\theta) = \sum_{v=0}^{n} \sum_{j=0}^{n-v} \frac{(-1)^j e^{v\theta}}{v!j!} = \sum_{g=0}^{n} \frac{(e^{\theta}-1)^g}{g!}.$$

From this expression it is easy to verify that

$$E(v) = 1, \qquad \sigma_v^2 = 1, \qquad E(v^{(r)}) = 1 \ (r \leq n).$$

It is interesting to observe that as n approaches infinity, the moment generating function approaches

$$\sum_{g=0}^{\infty} \frac{(e^\theta - 1)^g}{g!} = e^{(e^\theta - 1)}. \tag{9}$$

It therefore follows that the limiting form of the distribution is the Poisson distribution with parameter unity, namely,

$$\frac{e^{-1}1^x}{x!} = \frac{1}{e}\frac{1}{x!}. \tag{10}$$

If one writes the moment generating function as

$$\varphi(\theta) = \sum_{g=0}^{n} \frac{\left(\frac{\theta}{1!} + \frac{\theta}{2!} \div \cdots\right)^g}{g!} \tag{11}$$

one can see that the first n powers of θ in (9) are the same as in (11). Hence, the first n moments of the distribution (8) are the same as those of the Poisson distribution (10). In particular it is interesting to observe that in the random pairing of any two series, such as the serial numbers and order numbers in the Selective Service drawing, the expected number of matchings is exactly 1.

In applications of this method of matching (e.g., matching individuals and handwriting), the experiment may be repeated several times. It would be desirable, therefore, to have the probability law of the mean of a sample. The exact distribution, however, is too complicated to use. It follows from the central limit theorem that the mean of a sample of N observations from this distribution is asymptotically normally distributed as $N \to \infty$. It can also be shown by using the moment generating function that if the observations are from distributions with different n (i.e., the i-th observation from a pair of decks of n_i cards, $n_i \geq 2$), the distribution of the mean of the sample is asymptotically normal.

Now let us consider the analogue for three decks of cards. The generating function [1] for the number of matchings of three cards, one from each of three decks of arbitrary composition as defined in §3 is

$$(x_1y_1z_1e^\theta + x_1y_1z_2 + \cdots + x_1y_2z_1 + \cdots + x_2y_1z_1 + \cdots + x_2y_2z_2e^\theta + \cdots + x_ky_kz_ke^\theta)^n.$$

The probability of obtaining t matched triplets found after expanding this expression is

$$P(t) = \frac{\prod_{\alpha=1}^{3}\prod_{i=1}^{k} n_{\alpha i}!}{(n!)^3} \sum_{g=0}^{n-t} \binom{n}{t}\binom{n-t}{g}(-1)^{n-t-g} T_g, \tag{12}$$

where

$$T_g = \sum \frac{(g!)^3(n-g)!}{\prod_{i=1}^{k}\left[\prod_{\alpha=1}^{3}(n_{\alpha i}-s_i)!\cdot s_i!\right]},$$

where

$$\sum_{i=1}^{k} s_i = n - g, \qquad s_i \geq 0,$$

$$n_{\alpha i} - s_i \geq 0 \quad (\alpha = 1, 2, 3; i = 1, 2, \cdots, k).$$

To specialize (12) for the case to be considered here, namely, three identical decks of n different cards each, we let

$$n_{\alpha i} = 1 \qquad (\alpha = 1, 2, 3; i = 1, 2, \cdots, k),$$
$$n = k.$$

Then, observing that

$$T_g = (g!)^2 n!,$$

one finds that the probability of t matchings is

$$P(t) = \frac{1}{n!t!}\sum_{g=0}^{n-t}\frac{(-1)^{n-t-g}g!}{(n-t-g)!} = \frac{1}{n!t!}\sum_{j=0}^{n-t}\frac{(-1)^j(n-t-j)!}{j!}. \tag{13}$$

The moment generating function is

$$\varphi(\theta) = \frac{1}{n!}\sum_{t=0}^{n}\sum_{j=0}^{n-t}\frac{e^{t\theta}(-1)^j(n-t-j)!}{t!j!} \tag{14}$$

$$= \frac{1}{n!}\sum_{g=0}^{n}\frac{(n-g)!}{g!}(e^{\theta}-1)^g.$$

One can readily verify that

$$E(t) = \frac{1}{n}, \tag{15}$$

$$\sigma_t^2 = \frac{n^2-n+1}{n^2(n-1)}.$$

Since both $E(t)$ and σ_t^2 approach 0, as n approaches infinity, by Tchebycheff's inequality we can see that the probability approaches 1 that there will be no matched triplet as n increases without bound. As in the case of two decks, the result that the mean of a sample from this population is asymptotically normally distributed follows from the central limit theorem.

For the general case of q identical decks each of n different cards we can gen-

eralize (13), (14), and (15) immediately. First, let us note that the probability of s matched cards for q decks of arbitrary composition is

$$P(s) = \frac{\prod_{\alpha=1}^{q}\prod_{i=1}^{k} n_{\alpha i}!}{(n!)^q} \sum_{g=0}^{n-s} \binom{n}{s}\binom{n-s}{g}(-1)^{n-s-g} T_g,$$

where

$$T_g = \sum \frac{(g!)^q (n-g)!}{\prod_{i=1}^{k}\left[\prod_{\alpha=1}^{q}(n_{\alpha i}-s_i)!\cdot s_i!\right]},$$

where

$$\sum_{i=1}^{k} s_i = n - g, \qquad s_i \geq 0,$$

$$(n_{\alpha i} - s_i) \geq 0$$

$$(\alpha = 1, 2, \cdots, q;\ i = 1, 2, \cdots, k).$$

The probability of w, the number of matchings when each of the q decks consists of n different cards, is

$$P(w) = \frac{1}{(n!)^{q-2}} \sum_{j=0}^{n-w} \frac{(-1)^j[(n-w-j)!]^{q-2}}{j!}.$$

The moment generating function is

$$\frac{1}{(n!)^{q-2}} \sum_{g=0}^{n} \frac{[(n-g)!]^{q-2}}{g!}(e^\theta - 1)^g.$$

Finally, the mean and variance are

$$E(w) = \frac{1}{n^{q-2}},$$

$$\sigma_w^2 = \frac{n^{q-2}(n-1)^{q-2} + n^{q-2} - (n-1)^{q-2}}{n^{2(q-2)}(n-1)^{q-2}}.$$

5. Summary. Two distinct problems associated with card matching have been considered in this paper. In the first place it has been shown that the distribution of the number of matched pairs obtained under conditions of random pairing of two decks of arbitrary composition is asymptotically normal when the number of cards in each deck approaches infinity and the proportion of cards in each suit remains fixed. This demonstration was extended to the cases of matchings between three or more decks. The second problem treated in the present paper is concerned with the matchings between identical decks, each of n different cards. The probability law for the case of two decks was derived by

the use of a generating function. When n approaches infinity the limiting distribution was shown to be Poisson. The case of three or more decks was treated in similar manner, with the probability law and the moments given.

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[2] F. Yates, "Contingency tables involving small numbers and the χ^2-test", *Jour. Roy. Stat. Soc.* (*Supple.*), Vol. 1 (1934), pp. 217–235.

[3] D. Chapman, "The statistics of the method of correct matchings", *Amer. Jour. Psych.*, Vol. 46 (1934), pp. 287–298.

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NOTES

This section is devoted to brief research and expository articles, notes on methodology and other short items.

THE DETECTION OF DEFECTIVE MEMBERS OF LARGE POPULATIONS

By Robert Dorfman

Washington, D. C.

The inspection of the individual members of a large population is an expensive and tedious process. Often in testing the results of manufacture the work can be reduced greatly by examining only a sample of the population and rejecting the whole if the proportion of defectives in the sample is unduly large. In many inspections, however, the objective is to eliminate all the defective members of the population. This situation arises in manufacturing processes where the defect being tested for can result in disastrous failures. It also arises in certain inspections of human populations. Where the objective is to weed out individual defective units, a sample inspection will clearly not suffice. It will be shown in this paper that a different statistical approach can, under certain conditions, yield significant savings in effort and expense when a complete elimination of defective units is desired.

It should be noted at the outset that when large populations are being inspected the objective of eliminating all units with a particular defect can never be fully attained. Mechanical and chemical failures and, especially, man-failures make it inevitable that mistakes will occur when many units are being examined. Although the procedure described in this paper does not directly attack the problem of technical and psychological fallibility, it may contribute to its partial solution by reducing the tediousness of the work and by making more elaborate and more sensitive inspections economically feasible. In the following discussion no attention will be paid to the possibility of technical failure or operators' error.

The method will be described by showing its application to a large-scale project on which the United States Public Health Service and the Selective Service System are now engaged. The object of the program is to weed out all syphilitic men called up for induction. Under this program each prospective inductee is subjected to a "Wasserman-type" blood test. The test may be divided conveniently into two parts:

1. A sample of blood is drawn from the man,
2. The blood sample is subjected to a laboratory analysis which reveals the presence or absence of "syphilitic antigen." The presence of syphilitic antigen is a good indication of infection.

When this procedure is used, N chemical analyses are required in order to detect all infected members of a population of size N.

The germ of the proposed technique is revealed by the following possibility. Suppose that after the individual blood sera are drawn they are pooled in groups

of, say, five and that the groups rather than the individual sera are subjected to chemical analysis. If none of the five sera contributing to the pool contains syphilitic antigen, the pool will not contain it either and will test negative. If, however, one or more of the sera contain syphilitic antigen, the pool will contain it also and the group test will reveal its presence.[1] The individuals making up the pool must then be retested to determine which of the members are infected. It is not necessary to draw a new blood sample for this purpose since sufficient blood for both the test and the retest can be taken at once. The chemical analyses require only small quantities of blood.

Two questions arise immediately:

1. Will the group technique require fewer chemical analyses than the individual technique and, if so, what is the extent of the saving; and
2. What is the most efficient size for the groups?

Both questions are answered by a study of the probability of obtaining an infected group. Let

p = the prevalence rate per hundred, that is the probability that a random selection will yield an infected individual. Then

$1 - p$ = the probability of selecting at random an individual free from infection. And

$(1 - p)^n$ = the probability of obtaining by random selection a group of n individuals all of whom are free from infection. Then

$p' = 1 - (1 - p)^n$ = the probability of obtaining by random selection a group of n with at least one infected member.

Further

N/n = the number of groups of size n in a population of size N, so

$p'N/n$ = the expected number of infected groups of n in a population of N with a prevalence rate of p.

The expected number of chemical analyses required by the grouping procedure would be

$$E(T) = N/n + n(N/n)p'$$

or the number of groups plus the number of individuals in groups which require retesting.[2] The ratio of the number of tests required by the group technique to the number required by the individual technique is a measure of its expected relative cost. It is given by:

$$C = T/N = 1/n + p'$$

$$= \frac{n+1}{n} - (1 - p)^n.$$

---

[1] Diagnostic tests for syphilis are extremely sensitive and will show positive results for even great dilutions of antigen.

[2] The variance of T is $\sigma_T^2 = nNp'(1 - p') = nN[(1 - p)^n - (1 - p)^{2n}]$. The coefficient of variation of T becomes small rapidly as N increases.

The extent of the savings attainable by use of the group method depends on the group size and the prevalence rate. Figure 1 shows the shape of the relative cost curve for five prevalence rates ranging from .01 to .15.[3] For a prevalence rate of .01 it is clear from the chart that only 20% as many tests would be required by group tests with groups of 11 than by individual testing. The attainable savings decrease as the prevalence rate increases, and for a prevalence rate of .15, 72% as many tests are required by the most efficient grouping as by individual testing. The optimum group size for a population with a known prevalence rate is the integral value of n which has the lowest corresponding value on the relative cost curve for that prevalence rate.

TABLE I

Optimum Group Sizes and Relative Testing Costs for Selected Prevalence Rates

Prevalence Rate (per cent)	Optimum Group Size	Relative Testing Cost	Percent Saving Attainable
1	11	20	80
2	8	27	73
3	6	33	67
4	6	38	62
5	5	43	57
6	5	47	53
7	5	50	50
8	4	53	47
9	4	56	44
10	4	59	41
12	4	65	35
13	3	67	33
15	3	72	28
20	3	82	18
25	3	91	9
30	3	99	1

Optimum group sizes and their costs relative to the cost of individual testing are given in Table I for selected prevalence rates.

This table, together with the description of the group testing technique as it might be applied to blood tests for syphilis, reveals the two conditions for the economical application of the technique:

1. That the prevalence rate be sufficiently small to make worth while economies possible; and

[3] The prevalence rate of syphilis among the first million selectees and volunteers was .0185 for whites and .2477 for other races. Geographically, the prevalence rate for whites ranged from .0505 in Arizona to .0051 in Wisconsin. See Parran, Thomas and Vonderlehr, R. A., *Plain Words about Venereal Disease*, Reynal and Hitchcock, New York.

2. That it be easier or more economical to obtain an observation on a group than on the individuals of the group separately.

Where these conditions exist, it will be more economical to locate defective members of a population by means of group testing than by means of individual testing.

The principle of group testing may be applied to situations where the interest centers in the degree to which an imperfection is present rather than merely in its presence or absence. For example, it could be applied to lots of chemicals where it is desired to reject all batches with more than a certain degree of impurity. If n samples of a chemical are pooled and subjected to a single analysis, the degree of impurity in the pool will be the average of the impurities in the

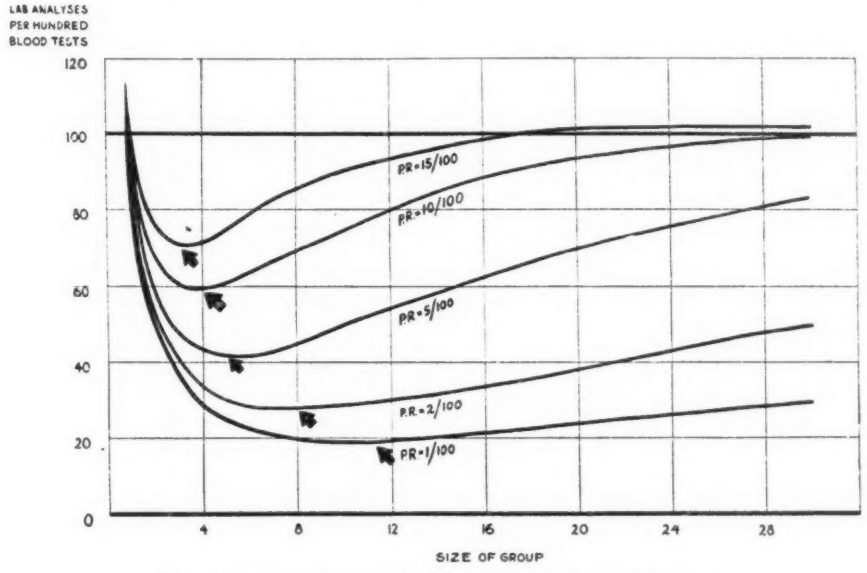

FIG. 1. Economies resulting from blood testing by groups
P.R. denotes prevalence rate

separate samples. If the criterion were adopted that the members of a pool would be examined individually whenever the proportion of impurity in the pool is greater than $1/n$-th the maximum acceptable degree of impurity, clearly no excessively impure batches would get by. The extent of the saving accomplished by this means can be computed by letting p' equal the probability that the pool will be impure enough to warrant retesting its constituent batches and using the formulas given above. The probability, p', can be calculated easily from the probability distribution of impurities in the separate batches.

It is evident that this approach will produce worthwhile savings only if the limit of acceptability is liberally above the per cent of impurity encountered in the bulk of the batches. It is also evident that under this scheme many of the

retests will indicate that all the batches in the pool are acceptable and that the retesting was not really needed. The criterion for retesting can be raised above $1/n$-th the limit of acceptability at the cost of a relatively small risk of accepting overly impure batches. The probability of failing to detect a defective batch when the retest criterion is raised in this manner will depend upon the form and parameters of the distribution of imperfection in single batches, as well as upon the number of batches in the pool. No simple general solution for this problem has been found.

FURTHER POINTS ON MATRIX CALCULATION AND SIMULTANEOUS EQUATIONS

By Harold Hotelling

Columbia University

Since the publication of "Some new methods in matrix calculation" in the *Annals of Mathematical Statistics* (March, 1943, pp. 1–34), the following relevant points have come to the attention of the author.

A. T. Lonseth has improved substantially the limit of error for the efficient method of inverting a matrix described on p. 14. He writes:

"Your use of the 'norm' of a matrix in the *Annals* paper especially interests me, as I was recently led to use it in solving the errors problem for infinite linear systems which are equivalent to Fredholm-type integral equations.

"It is possible to replace the term $p^{\frac{1}{2}}$ in your inequality (7.5) by one, so that

$$N(C_m - A^{-1}) \leqq N(C_0)k^{2^m}/(1 - k).$$

To see this, one observes that from the developments on the bottom of p. 13 it follows that $(I - D)^{-1} = I + D^*$, where $N(D^*) < k/(1 - k)$. Then

$$C_0(I - D)^{-1} = C_0 + C_0D^*$$

so that

$$N[C_0(I - D)^{-1}] \leqq N(C_0) + N(C_0)\,N(D^*) = N(C_0)\{1 + N(D^*)\},$$

from which the result stated is seen to follow. I happen to have noticed this because the same thing has cropped up often in my recent work, and for the infinite case a bound $p^{\frac{1}{2}}$ is no bound at all.

"Your paper has suggested improvements in my own proofs, for which I am grateful."

Dr. Lonseth's first formula above might well be written at the bottom of p. 14 of my article as a substitute for (7.5). It both simplifies and reduces the limit of error.

A method of solving normal equations by iteration, in which trial values of the unknown regression coefficients were applied to the values of the predictors

and predictand in each of the N cases, and the results were used to improve the trial values, was orally suggested by John C. Flanagan in 1934. The plan involved the use of punched cards for the N substitutions in the trial regression equation at each stage. However, it seemed on further consideration and discussion that this would involve an unnecessarily large amount of work, since other methods require only as many substitutions at each stage as the number of unknowns, which is always less than N and usually very much less. I believe that Dr. Flanagan thereupon abandoned this plan and never published it.

Louis I. Guttman has proposed a similar method,[1] and has provided a proof of convergence in certain cases. In a final section he shows that the method can be modified by applying the same type of iterations to the normal, or product-sum, matrix instead of to the matrix of observations. This modification avoids the difficulty mentioned above. It is stated that one of these methods has been applied to a 64-variable problem.

The first method of section 10 of my paper for solving sets of linear equations is equivalent, in the case of normal equations, to the second method of Dr. Guttman. It is regrettable that reference to his study was omitted.

R. D. Gordon believes that the inequalities for principal components obtained at the end of the paper can be improved, but his entry into the army has prevented his fully working out his ideas. Paul A. Samuelson has some new and as yet unpublished ideas relating to calculation of principal components.

Merrill M. Flood, in "A computational procedure for the method of principal components," *Psychometrika*, Vol. 5 (1940), pp. 169–172, presents a method which appears to have considerable value, in that the number of vector multiplications is relatively small. However it requires solution of a system of $p - 1$ linear equations for each latent vector determined, and also of an additional such system. The relative value of this and other methods may depend on the relative costs of vector multiplication and of solving systems of linear equations. This in turn depends on the mechanical facilities available.

Paul Horst's paper, "A method for determining the coefficients of a characteristic equation" (*Annals of Mathematical Statistics*, Vol. 6 (1935), pp. 83–84) should have been referred to in connection with sections 11 and 12.

On p. 23 of "Some new methods in matrix calculation," in the sixth line from the bottom, *smaller* should be replaced by *greater*. On p. 32, the last expression in the third line should have r_i^2 in place of r_i. The last displayed formula on this page should read

$$w_{1i} + \cdots + w_{ki} \geq 1 - \frac{\nu_{2i} - \nu_{1i}^2}{(\eta_{k+1} - \nu_{1i})^2},$$

and the subscript $r + 1$ in the next line should be $k + 1$.

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[1] "An iterative method for multiple correlation," *The Prediction of Personal Adjustment*, by Paul Horst and collaborators, Social Science Research Council, New York, 1941, pp. 313–318.

NEWS AND NOTICES

Readers are invited to submit to the Secretary of the Institute news items of general interest

Personal Items

Dr. Paul H. Anderson is Regional Statistician with the War Production Board and Lecturer in Mathematics at Western Reserve University.

Mr. Kenneth J. Arrow is a second lieutenant with the United States Army Air Forces.

Assistant Professor H. M. Bacon of Stanford University has been promoted to an associate professorship.

Dr. G. A. Baker of the College of Agriculture of the University of California has been promoted to an assistant professorship.

Mr. Blair M. Bennett is attached to the Operations Research Section of the Eighth Bomber Command.

Mr. Richard Berger is in the United States Army Air Forces.

Mr. John L. Carlson is a lieutenant in the United States Naval Reserve.

Mr. Edward P. Colman is a major in the Coast Artillery Corps and is stationed at West Point.

Mr. William F. Elkin has been appointed Research Secretary of the Philadelphia Tuberculosis and Health Association.

Professor R. A. Fisher, Galton Professor in the University of London since 1933, has been appointed to the chair of Genetics in Cambridge University.

Dr. J. P. Guilford is a lieutenant colonel in the Army Air Forces. He is chief of the Field Research Unit, Psychological Section of the Surgeon's Office with headquarters at Fort Worth.

Dr. Edward Helley of Monmouth Junior College has been appointed Visiting Lecturer at the Illinois Institute of Technology.

Dr. H. B. Mann has been appointed to an instructorship at Bard College, Columbia University.

Dr. Nilan Norris is a lieutenant in the Army Air Forces, and is serving as Statistical Officer.

Dr. Edwin G. Olds has been granted leave by Carnegie Institute of Technology to act as Chief Statistical Consultant to the Industrial Processes Branch of the Office of Production Research and Development, War Production Board.

Miss Ruth L. Owen has been commissioned as an ensign in the United States Naval Reserve. She is acting as Supply and Disbursing Officer for the Naval V-12 Unit at St. Lawrence University.

Mr. Robert W. Royston is a lieutenant in the United States Naval Reserve.

Dr. H. M. Schwartz has been appointed Assistant Professor of Mathematics at the University of Idaho.

Mr. William B. Simpson is now a member of the armed forces and is stationed at Camp Crowder.

Mr. Irvin Stein is an ensign in the United States Naval Reserve.

Mr. Milton S. Stevens is an apprentice seaman in the United States Naval Reserve.

Mr. W. A. Vezeau has been promoted to the rank of Assistant Professor of Mathematics at the University of Detroit.

Organization of Washington Chapter of the Institute

Professor Harold Hotelling of Columbia University spoke at George Washington University, November 19, 1943, under the auspices of the Institute of Mathematical Statistics before an audience of over 150 persons. The subject of his lecture was *Multivariate Statistical Analysis*. At the close of the lecture the Washington Chapter of the Institute was organized. A Planning Committee consisting of William G. Madow, Chairman, Meyer A. Girshick, and W. Edwards Deming was elected. Members of the Institute who are interested in being in contact with the Washington Chapter should write to William G. Madow, Bureau of Agricultural Economics, Department of Agriculture.

New Members

The following persons have been elected to membership in the Institute:

Belz, Asso. Prof. Maurice H. M.A. (Melbourne) Univ. of Melbourne, Carlton, N. 3, Victoria, Australia.

Capó, Bernardo G. Ph.D. (Cornell) Biometrician, Agric. Exp. Station, Rio Piedras, Puerto Rico, *32½ Rosario St., Santurce.*

Crawford, Elizabeth S. B.A. (Mundelein Coll.) Asso. Labor Market Analyst, War Manpower Commission. *935 Lincoln St., Denver, Colo.*

Crawford, James R. Div. Supervisor, Vega Aircraft Corp., *11626 Kittridge St., N. Hollywood, Calif.*

Hoffer, Prof. Irwin S. M.B.A. (Harvard) Temple Univ., Philadelphia, Pa., *Willow Ave., Ambler, Pa.*

Maynard, Burton I. A.B. (Stanford) Stat. Analyst and Stat., *11211 Brookhaven Ave., Los Angeles, Calif.*

Mazza, Prof. Sigfrido C. Dir., Instituto de Estadistica. Facultad de C. Economicas, *Tristan Narvaja 1474, Montevideo, Uruguay.*

Motock, George T. M.S. (Carnegie Inst. Tech., Ohio State) Dir. of Res., Republic Steel Corp., Cleveland, Ohio.

Neurath, Paul M. LL.D. (Vienna) Lecturer, Coll. of the City of New York, N. Y. *549 W. 113 St.*

Page, Warren H. B.A. (Queens Coll.) Pfc., U. S. Army, 3301 A.S.T.U. Virginia Polytechnic Inst., Blacksburg, Va.

Pearson, Prof. E. S. D.Sc. (London) University Coll., Gower St., London, W. C. 1, Eng.

Rock, Sibyl M. B.A. (California) Res. Asso., Consolidated Eng. Corp., *983 N. Holliston St., Pasadena, Calif.*

Rule, Wayne B. M.S. (Iowa) Sr. Analysis Clerk, Metropolitan Life Ins. Co., *29 Utopian Ave., Suffern, N. Y.*

Thompson, Walter H. M.S. (Iowa) Sgt., U. S. Army; Instr., Agric. Economics Dept., Virginia Polytechnic Inst., Blacksburg, Va.

Thomson, Prof. Godfrey H. D.Sc. (Durham) Dir. of the Training of Teachers, Univ. of Edinburgh, Edinburgh, Scotland.

REPORT ON THE NEW BRUNSWICK MEETING OF THE INSTITUTE

The Sixth Summer Meeting of the Institute of Mathematical Statistics was held at The New Jersey College for Women, Rutgers University, Sunday and Monday, September 12 and 13, 1943, in conjunction with the meetings of the American Mathematical Society and the Mathematical Association of America. The following fifty-two members of the Institute attended the meeting:

T. W. Anderson, H. E. Arnold, K. J. Arnold, L. A. Aroian, B. M. Bennett, E. E. Blanche, C. I. Bliss, A. H. Bowker, Hobart Bushey, W. G. Cochran, T. F. Cope, C. C. Craig, H. B. Curry, J. H. Curtiss, J. F. Daly, Mary Elveback, W. Feller, R. M. Foster, J. A. Greenwood, J. I. Griffin, C. C. Grove, F. E. Grubbs, E. J. Gumbel, Harold Hotelling, Tjalling Koopmans, H. G. Landau, Howard Levene, Simon Lopata, P. J. McCarthy, W. G. Madow, Margaret Martin, J. W. Mauchly, E. B. Mode, L. F. Nanni, C. O. Oakley, P. S. Olmstead, F. E. Satterthwaite, Bernice Scherl, H. M. Schwartz, L. W. Shaw, J. Shohat, Blanche Skalak, Mortimer Spiegelman, Arthur Stein, H. W. Steinhaus, A. W. Tucker, J. W. Tukey, D. F. Votaw, Abraham Wald, S. S. Wilks, Jacob Wolfowitz, Bertram Yood.

Professor S. S. Wilks of Princeton University acted as chairman for the Sunday morning session. The following papers were presented:

1. *Some New Statistical Applications of Partitioned Matrices and Iterative Methods.*
   Harold Hotelling, Columbia University
2. *On the Construction of Orthogonal Latin Squares.*
   Henry B. Mann, Columbia University

Dr. Jacob Wolfowitz, Columbia University, presided at the session on Sunday afternoon. At this session the following papers were presented:

1. *Recent Developments in the Statistical Analysis of Problems Requiring the Use of Vector Variates.*
   W. G. Madow, Office of Price Administration.
2. *Statistical Inference when the Form of the Distribution Function is Unknown.*
   Henry Scheffé, Princeton University.

The session on Monday morning was held jointly with the American Mathematical Society. Professor C. C. Craig, University of Michigan, acted as chairman, and the following contributed papers were read:

1. *Asymptotic Distributions of Ascending and Descending Runs.*
   Jacob Wolfowitz, Columbia University.
2. *On the Plotting of Statistical Observations.*
   E. J. Gumbel, New School for Social Research.
3. *On a Measure-Theoretic Problem Arising in the Theory of Non-Parametric Tests.*
   (Read by title.)
   Henry Scheffé, Princeton University.
4. *On a General Class of "Contagious" Distributions.*
   Will Feller, Brown University.
5. *On the Statistical Treatment of Linear Stochastic Difference Equations.*
   H. B. Mann and Abraham Wald, Columbia University.
6. *An Exact Test for Randomness in the Non-Parametric Case Based on Serial Correlation.*
   Abraham Wald and Jacob Wolfowitz, Columbia University.

On Saturday afternoon the members of the three societies were the guests of Miss Margaret Trumbull Corwin, Dean of the College, New Jersey College for Women, at an informal reception at the Dean's House. On Sunday evening an informal buffet supper for the mathematical organizations was served at Wood Lawn, the Alumnae House of the New Jersey College for Women. Later the same evening the Department of Music presented a Musicale in the Music Building.

EDWIN G. OLDS,
Secretary

REPORT ON THE SECOND MEETING OF THE PITTSBURGH CHAPTER OF THE INSTITUTE

The second meeting of the Pittsburgh Chapter of the Institute of Mathematical Statistics was held at Carnegie Union, Carnegie Institute of Technology, on Saturday, October 9, 1943. Thirty-four persons attended the meeting, including the following eight members of the Institute:

W. O. Clinedinst, G. G. Eldredge, K. L. Fetters, H. J. Hand, G. E. Niver, F. G. Norris, E. G. Olds, E. M. Schrock.

At the morning session Mr. Charles E. Young, Westinghouse Electric and Manufacturing Company, presented a paper entitled "Analysis of Cyclical Fluctuations." The program for the afternoon session consisted of a paper entitled "Use of orthogonal coordinates in linear regression," presented by Mr. W. O. Clinedinst, National Tube Company. Mr. F. G. Norris, President of the Pittsburgh Chapter, acted as chairman for both sessions.

HOWARD HAND,
Secretary of the Pittsburgh Chapter

ABSTRACTS OF PAPERS

(Presented Monday, September 13, 1943, at the New Brunswick Meeting of the Institute)

Asymptotic Distributions of Ascending and Descending Runs. JACOB WOLFOWITZ, Columbia University.

Let $a_1, a_2, \cdots, a_N$ be any permutation of N unequal numbers. Let there be assigned to each permutation the same probability. An element $a_i (1 < i < N)$ is called a turning point if a_i is greater than or less than both a_{i-1} and a_{i+1}. Let a_j and a_{j+k} be consecutive turning points; they are said to determine a "run" of length k. The author obtains the asymptotic distributions of a large class of functions of these runs. An example of his results is the following: It is proved that the following are asymptotically normally distributed: (a) the total number of runs; (b) $R(p)$, the number of runs of length p; (c) $R(p)$ and $R(q)$ jointly. Similar results are obtained for runs defined by any of a large set of criteria, of which the one given above is of value in statistical applications.

On the Plotting of Statistical Observations. E. J. GUMBEL, The New School for Social Research.

It is well known that there exist two step functions corresponding to a continuous variate. We may attribute to the m-th observation the ranks m or $m - 1$. To obtain one and only one serial number m, which will, in general, not be integer, we attribute to x_m an adjusted frequency $m - \Delta$, namely the probability of the most probable m-th value. The correction Δ for the rank thus introduced depends upon the distribution. If the variate is unlimited and possesses a mode, Δ increases for increasing values of the variate from zero up to unity. The correction is important for small numbers of observations. For large numbers of observations and for the ogive it is sufficient to choose $\Delta = \frac{1}{2}$. The calculation of Δ allows a correct plotting of all observations (including the first and last) on probability paper (equiprobability test). For the return periods, the ranks m and $m - 1$ correspond to the observed exceedance and recurrence intervals. The correction Δ leads to adjusted return periods which pass for increasing values of the variate from the exceedance to the recurrence intervals, provided the variate is unlimited and possesses a single mode. The asymptotic standard error of the partition values may be used to construct confidence bands for the ogive, the equiprobability test, and the return periods. This control for the fit between theory and observation may be applied to all observations which are not extreme.

On a Measure-Theoretic Problem Arising in the Theory of Non-Parametric Tests. HENRY SCHEFFÉ, Princeton University.

Let $F(x)$ be the cumulative distribution function of a univariate population. Denote a sample from the population by the sample point, $E = (x_1, x_2, \cdots, x_k)$ and let w be a Borel region in the sample space. How can we characterize w in order that $Pr\{E \text{ in } w\}$ be independent of $F(x)$ for all F in a given class of distribution functions? For various classes of F necessary conditions and sufficient conditions are found. For example, if the boundary of w is a null set, a necessary and sufficient condition for w to have the desired property for all absolutely continuous $F(x)$ is that it have the following structure except on a null set: For every point E in the sample space, M of the $k!$ points obtained by permuting the coordinates of E are in w and the remaining $k! - M$ are not $(0 < M < k!)$.

On a General Class of "Contagious" Distributions. W. FELLER, Brown University.

This paper is concerned with some properties of a class of contagious distributions which contains, among others, some distributions studied by Greenwood and Yule, Polya, and Neyman, respectively.

On the Statistical Treatment of Linear Stochastic Difference Equations. H. B. MANN AND A. WALD, Columbia University.

For any integer t let $x_{1t}, \cdots, x_{rt}$ be a set of r random variables which satisfy the system of linear stochastic difference equations $\sum_{j=1}^{r} \sum_{k=0}^{p_{ij}} \alpha_{ijk} x_{j,t-k} + \alpha_i = \epsilon_{it}$ $(i = 1, \cdots, r)$. The coefficients α_{ijk} and α_i are (known or unknown) constants and the vectors $\epsilon_t = (\epsilon_{1t}, \cdots, \epsilon_{rt})$ $(t = 1, 2, \cdots,$ ad inf.) are independently distributed random vectors each having the same distribution. It is assumed that $E(\epsilon_{it}) = 0$. The problem dealt with in this paper is to estimate the unknown coefficients α_{ijk} and α_i on the basis of Nr observations x_{it} $(i = 1, \cdots, r; t = 1, \cdots, N)$. The statistics used as estimates of the unknown coefficients are identical

with the maximum likelihood estimates if ϵ_i is normally distributed. The joint limiting distribution of these estimates is obtained without assuming normality of the distribution of ϵ_i.

An Exact Test for Randomness in the Non-Parametric Case Based on Serial Correlation. A. WALD AND J. WOLFOWITZ, Columbia University.

Let $X_1, \cdots, X_n$ be n chance variables, about the distribution of which nothing is known. Let the problem be to test the (null) hypothesis that $X_1, \cdots, X_n$ are independently distributed with the same distribution function. It is shown that an exact test of this hypothesis based on the serial correlation coefficient can be made. For this purpose the distribution of the serial correlation coefficient in the sub-population consisting of all possible permutations of the observed values is employed. Under the null hypothesis, this distribution is independent of the distribution function of $X_i (i = 1, \cdots, n)$. Several exact moments are obtained and asymptotic normality is proved.

DIRECTORY OF THE INSTITUTE OF MATHEMATICAL STATISTICS[1]

(As of October 1, 1943)

(The names of Fellows of the Institute are designated by *)

Acerboni, Prof. Argentino V. Dr. Ec. (Buenos Aires) Facultad de C. Economicas, Buenos Aires, Argentina. *Larroque 232, Banfield, Argentina.*

Alt, Franz L. Ph.D. (Vienna) U. S. Army. *271 Fort Washington Ave., New York, N. Y.*

Alter, Dinsmore Col., CAC, Fort Mason, San Francisco, Calif.

Anderson, Paul H. Ph.D. (Illinois) Regional Stat., WPB; Lecturer, Western Reserve Univ., Cleveland, Ohio. *8414 Brookline.*

Anderson, Asst. Prof. Richard L. Ph.D. (Iowa State Coll.) North Carolina State Coll. Exp. Sta., Raleigh, N. C.

Anderson, Theodore W., Jr. M.A. (Princeton) Instr., Princeton Univ., Princeton, N. J.

Anthony, Lucius U. S. Army. *Woodinville, Wash.*

Arias B., Jorge C.E. (Guatemala) 3 Avenida Sur 65, Guatemala City, Guatemala, Central America.

Arnold, Asso. Prof. Herbert E. Ph.D. (Yale) Wesleyan Univ., Middletown, Conn.

Arnold, Asst. Prof. Kenneth J. Ph.D. (Mass Inst. Tech.) Univ. of New Hampshire, Durham, N. H.

Aroian, Leo A. Ph.D. (Michigan) Instr., Hunter Coll., New York, N. Y.

Arrow, Kenneth J. M.A. (Columbia) 2nd Lt., USAAF, Weather Information Service, Pentagon Bldg., Washington, D. C. *1416 Nicholson St., NW.*

Bachelor, Robert W. M.B.A. (Washington) Asst. Dir., Res. Council, American Bankers Assn., New York, N. Y.

Bacon, Asso. Prof. Harold M. Ph.D. (Stanford) Stanford Univ., Stanford University, Calif. *Box 1144.*

Bailey, A. L. B.S. (Michigan) Stat., American Mutual Alliance, 60 E. 42 St., New York, N. Y.

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